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(54) Title: NUCLEIC ACIDS ENCODING PROTEIN KINASES

(57) Abstract: Nucleic acids encoding protein kinases are disclosed, and methods of using same.

NUCLEIC ACIDS ENCODING PROTEIN KINASES

RELATED APPLICATIONS

This application claims the benefit of and priority to U.S Provisional Application 60/301,098, filed June 26, 2001 and to U.S. Provisional Application 60/332,870, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

Protein kinases are enzymes that catalyze the phosphorylation of target protein substrates. The phosphorylation is usually a transfer reaction of a phosphate group from ATP to the protein substrate.

At least 400 enzymes have been identified as protein kinases. The specific structure in the target substrate to which the phosphate is transferred is frequently a tyrosine, serine or threonine residue, and such protein kinase enzymes are commonly referred to as tyrosine kinases or serine/threonine kinases. Another class of protein kinases phosphorylates histidine residues. Most protein kinases recognize a simple amino acid motif associated with a nearby residue.

The phosphorylation reactions, and counteracting phosphatase reactions, are involved in countless cellular processes that underlie responses to diverse intracellular signals (typically mediated through cellular receptors), regulation of cellular functions, and activation or deactivation of cellular processes. A cascade of protein kinases often participate in intracellular signal transduction and are necessary for the realization of these cellular processes. Because of their ubiquity in these processes, the protein kinases can be found as an integral part of the plasma membrane or as cytoplasmic enzymes or localized in the nucleus, often as components of enzyme complexes. In many instances, these protein kinases are an essential element of enzyme and structural protein complexes that determine where and when a cellular process occurs within a cell.

Protein kinases are regulated by a variety of mechanisms. Some protein kinases are constitutively active, while others are activated by the binding of a messenger (cAMP-dependent protein kinase, *e.g.*, protein kinase A; cGMP-dependent protein kinase; protein kinase C). Some are activated by calcium and calmodulin (*e.g.*, Ca^{2+}/calmodulin-dependent protein kinase II, phosphorylase kinase, myosin light chain kinase, elongation factor 2 kinase). Protein kinases that

are activated by such a messenger tend to regulate most or all of the intracellular responses to the messenger.

Other protein kinases are activated by an extracellular signal, and are also called the receptor protein kinases (*e.g.*, polypeptide hormones receptors, growth factors, insulin, epidermal growth factor, platelet-derived growth factor). The catalytic domain of such protein kinases is also the cytoplasmic domain of a transmembrane receptor, the the extracellular domain binds an extracellular messenger. Binding to the domain activates the protein kinase inside the membrane.

Finally, some protein kinases are in turn regulated by other protein kinases, and multiple such relationships between protein kinases can exist, forming a protein kinase cascade, in which each protein kinase phosphorylates the next. Such kinases include, *e.g.*, cAMP-dependent protein kinase, AMP-activated protein kinase, MAP kinase kinase kinase, MAP kinase kinase, MAP kinase and S6 kinase.

SUMMARY OF THE INVENTION

The present invention relates to human protein kinase genes, particularly nucleic acids comprising protein kinase genes, and the amino acids encoded by such nucleic acids. These genes are shown in Tables I and II and the sequence listing. In Tables I and II, each kinase entry lists the name (*e.g.*, "MOOSE03013"), the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14435"), and the exon locations (*e.g.*, "1134827 . . 1135076, . .").

Sub-family information on the sequences is shown in Table III. For each sequence, the following information is provided: the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14435"), the name (*e.g.*, "MOOSE03013"), and the subfamily to which the sequence appears to belong. The assignments were made on the basis of the best E-value with which the sequence aligned.

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*, cDNA

molecules) encoding a protein kinase polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs: 1-80 (even numbers).

The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a protein kinase in a sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a protein kinase polypeptide (*e.g.*, one of SEQ ID NOs: 1-80 (even numbers, or the complement of one of SEQ ID NOs: 1-80 (even numbers); a nucleotide sequence encoding one of SEQ ID NOs: 1-80 (odd numbers), or a fragment or derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a protein kinase polypeptide, or fragment or derivative thereof, comprising detecting (directly or indirectly) the level of expression of the protein kinase polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for preparing a polypeptide encoded by an isolated nucleic acid molecule described herein (a protein kinase polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule.

The invention further provides an isolated polypeptide encoded by isolated nucleic acid molecules of the invention (*e.g.*, protein kinase polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers). The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers), preferably about 95, 96, 97, 98 or 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by a protein kinase. The methods of diagnosing such a predisposition in an individual include detecting the presence of a mutation in a

protein kinase, as well as detecting alterations in expression of a protein kinase polypeptide, such as the presence of different splicing variants of protein kinase polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter (*e.g.*, enhance or inhibit) the activity or expression of one or more protein kinase polypeptides. For example, a cell, cellular fraction, or solution containing a protein kinase polypeptide or a fragment or derivative thereof, can be contacted with an agent to be tested, and the level of protein kinase polypeptide expression or activity can be assessed. The activity or expression of more than one protein kinase polypeptide can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one type of protein kinase polypeptide, such as different splicing variants, and the levels of the different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides which interact with one or more protein kinase polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a protein kinase polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the protein kinase polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a protein kinase polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector under appropriate conditions allows identification of polypeptides which interact with the protein kinase polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of a protein kinase polypeptide.

Agents that enhance or inhibit protein kinase polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or inhibiting) protein kinase polypeptide expression or activity by contacting a cell containing protein kinase and/or polypeptide, or by contacting the protein kinase polypeptide, with an agent that enhances or inhibits expression or activity of protein kinase or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents that alter activity of protein kinase polypeptide. The invention

further pertains to methods of treating conditions mediated by protein kinases, by administering protein kinase therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of protein kinase polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of protein kinase polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising protein kinases, and the protein kinase amino acids encoded by those nucleic acids.

Protein kinases are involved in regulation of cellular functions, and activation or deactivation of cellular processes, and many of the cellular processes in response to intracellular signals. Cascades of protein kinases often participate in intracellular signal transduction and are necessary for the realization of these cellular processes.

Protein kinases are the major modes through which extracellular signal molecules produce intracellular effects. They are also involved in stress responses, and protect the cell against changes in metabolite levels that would otherwise be toxic to the cell. They are also the major way in which mechanisms such as DNA synthesis and mitosis are timed.

The receptor tyrosine kinases comprise a large family of transmembrane receptors with diverse biological activities. At least nineteen distinct receptor tyrosine kinase subfamilies have been identified. This family includes receptors that are crucial for the growth and differentiation of a variety of cell types (Yarden and Ullrich, *Ann. Rev. Biochem.* 57:433-478 (1988); Ullrich and Schlessinger, *Cell* 61:243-254 (1990)). The intrinsic function of receptor tyrosine kinases is activated upon ligand binding, which results in phosphorylation of the receptor and multiple cellular substrates, and subsequently in a variety of cellular responses (Ullrich & Schlessinger, *Cell* 61:203-212 (1990)). Thus, receptor tyrosine kinase-mediated signal transduction is initiated by extracellular interaction with a specific growth factor (ligand), typically followed by receptor dimerization, stimulation of the intrinsic protein tyrosine kinase activity and receptor trans-phosphorylation. Binding sites are thereby created for intracellular signal transduction molecules and lead to the formation of complexes with a spectrum of cytoplasmic signaling molecules that facilitate the appropriate cellular response (*e.g.*, cell division, differentiation, metabolic effects, changes in the extracellular microenvironment).

Several receptor tyrosine kinases such as FGFR-1, PDGFR, TIE-2 and c-Met, and growth factors that bind them, have been suggested to play a role in

angiogenesis, although some may promote angiogenesis indirectly (Mustonen and Alitalo, *J. Cell Biol.* 129:895-898 (1995)). One such receptor tyrosine kinase, known as fetal liver kinase 1 (FLK-1), is a member of the type III subclass of RTKs. An alternative designation for human FLK-1 is a kinase insert domain-containing receptor (KDR) (Terman *et al.*, *Oncogene* 6:1677-83 (1991)). Another alternative designation for FLK-1/KDR is vascular endothelial cell growth factor receptor 2 (VEGFR-2), since it binds VEGF with high affinity. The murine version of FLK-1/VEGFR-2 has also been called NYK (Oelrichs *et al*, *Oncogene* 8(1):11-15 (1993)). DNAs encoding mouse, rat and human FLK-1 have been isolated, and the nucleotide and encoded amino acid sequences reported (Matthews *et al.*, *Proc. Natl. Acad. Sci. USA* 88:9026-30 (1991); Terman *et al.*, 1991, *supra*; Terman *et al.*, *Biochem. Biophys. Res. Comm.* 187:1579-86 (1992); Millauer *et al.*, *Cell* 72:835-846 (1993)). Numerous studies such as those reported in Millauer *et al.*, *supra*, suggest that VEGF and FLK-1/KDR/VEGFR-2 are a ligand-receptor pair that play an important role in the proliferation of vascular endothelial cells, and formation and sprouting of blood vessels, termed vasculogenesis and angiogenesis, respectively.

Protein tyrosine kinases catalyse the phosphorylation of specific tyrosine residues in cellular proteins, and this post-translational modification of these substrate proteins, which can be enzymes themselves, acts as a molecular switch regulating cell proliferation, activation or differentiation (for review, see Schlessinger and Ullrich, *Neuron* 9:383-391 (1992)). Aberrant or excessive protein tyrosine kinase activity has been observed in many disease states including benign and malignant proliferative disorders as well as diseases resulting from inappropriate activation of the immune system (*e.g.*, autoimmune disorders), allograft rejection, and graft vs. host disease. In addition, endothelial-cell specific receptor protein tyrosine kinases such as KDR and Tie-2 mediate the angiogenic process, and are thus involved in supporting the progression of cancers and other diseases involving inappropriate vascularization. Angiogenesis-mediated diseases include, but are not limited to, cancers, solid tumors, blood-born tumors (*e.g.*, leukemias), tumor metastasis, benign tumors (*e.g.*, hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), infantile hemangiomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases (*e.g.*, diabetic retinopathy, retinopathy of prematurity, choroidal neovascularization due to age-related macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularization, telangiectasia, hemophiliac joints, angiofibroma, and wound granulation.

Some intracellular protein kinases specifically interact with various members of the G protein-coupled receptor superfamily, and are able to desensitize them and thereby weaken the signal or prevent it from being effected. The G protein-coupled receptors are involved in the transmission of signals that originate from low molecular weight ligands such as adrenaline or from peptide ligands such as chemokines and a variety of hormones such as melanocyte stimulating hormone (MSH). So far, six of these kinases have been discovered (GRK1 through GRK6). Some of the GRKs are restricted to a small number of tissues (*e.g.*, GRK-1), while GRK2 and 3, known also as βARK1 and βARK2, are ubiquitously expressed. A comprehensive review is provided, for example, by M. Bunemann and M.M. Hosey, "G-Protein Coupled Receptor Kinases as Modulators of G-Protein Signalling," *J. of Physiology, Vol. 517(1):*5-23 (1999). Methods and substances that modulate (increase or decrease) the function of 7TM receptors could be used to treat a wide variety of diseases and conditions associated with 7TM receptor function. G protein-coupled receptors, for instance, are involved in an enormous range of biological processes, and have been found to regulate such processes as hydrolysis of plasma membrane phospholipids, the K^+ and Ca^{2+} ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (*e.g.*, pituitary, adrenal, ovarian). Many drugs bind to a G protein-coupled receptor and either produce a response or block the actions of the normal signal. The GPCR superfamily includes the receptors for many important signaling pathways, including, but not limited to, hormone receptors, growth factors, viral receptors, neuroreceptors, etc., such as acetylcholine, adrenocorticotropin (ACTH), adenosine, α-adrenergic receptors, β-adrenergic receptors, angiotensin, bombesin, bradykinin, C5a, calcitonin, cAMP, cannabinoid, C-C chemokine, cholecystokinin/gastrin (CCK/gastrin), cytomegalovirus, dopamine, endothelial differentiation gene-1, endothelin, formyl peptide, glutamate (metabotropic), gonadotropin-releasing hormone, growth hormone-releasing hormone, histamine, 5-hydroxytryptamine, interleukin-8, kinin, luteinizing hormone/follicle-stimulating hormone/thyroid-stimulating hormone (LH/FSH/TSH), mas, melanocortin, muscarinic, neuropeptide Y, neurotensin, odorant, opioid, opsins, parathyroid hormone, platelet-activating factor (PAF), prolactin, prostaglandin E, rhodopsins, secretin, serotonin, somatostatin, tachykinin, taste, testis specific, thrombin, thromboxine A_2, thyrotropin-releasing hormone (TRH), tyramine/octopamine, vasoactive intestinal peptide (VIP), vasopressin, viral and yeast mating factor.

These receptors are involved in the treatment of infections and various diseases and conditions, including, but not limited to, bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; cancers; diabetes; asthma; Parkinson's disease; both acute and congestive heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy (benign prostatic hyperplasia); chronic renal failure; renal disease; impaired glucose tolerance; seizure disorder; depression; anxiety; obsessive compulsive disorder; affective neurosis/disorder; depressive neurosis/disorder; anxiety neurosis; dysthymic disorder; behavior disorder; mood disorder; shizophrenia; psychosexual dysfunction; sex disorder; sexual disorder; disturbed biological and circadian rhythms; feeding disorders, such as anorexia, bulimia, cachexia, and obesity; Cushing's syndrome/disease; basophil adenoma; prolactinoma; hyperprolactinemia; hypopituitarism; hypophysis tumor/adenoma; hypothalamic diseases; Froehlich's syndrome; adenohypophysis disease; hypophysis disease; hypophysis tumor/adenoma; pituitary growth hormone; adenohypophysis hypofunction; adrenohpophysis hyperfuunction; hypothalamic hypogonadism; Kallman's syndrome (anosmia, hyposmia); functional or psychogenic amenorrhea; hypopituitarism; hypothalamic hypothyroidism; hypothalamic-adrenal dysfunctions; idiopathic hyperprolactinemia; hypothalamic disorders of growth hormone deficiency; idiopathic growth hormone deficiency; dwarfism; gigantism; acromegaly; disturbed biological and circadian rhythms; and sleep disturbances associated with such diseases as neurological disorders, heart and lung diseases, mental illness, and addictions; migraine; hyperalgesia; enhanced or exaggerated sensitivity to pain, such as hyperlgesia, causalgia and allodynia; acute pain; burn pain; atypical facial pain; neuropathic pain; back pain; complex regional pain syndromes I and II; arthritic pain; sports injury pain; pain related to infection, *e.g.*, HIV, post-polio syndrome, and post-herpetic neuralgia; phantom limb pain; labour pain; cancer pain; post-chemotherapy pain; post-stroke pain; post-operative pain; neuralgia; and tolerance to narcotics or withdrawal from narcotics; sleep disorders; sleep apnea; narcolepsy; insomnia; parasomnia; jet-lag syndrome; and other neurodegenerative disorders, which includes nosological entities such as disinhibition-dementia-parkinsonism-amyotrophy complex; pallido-ponto-nigral degeneration; and dyskinesias, such as Huntington's disease or Gilles dela Tourett's syndrome.

With the availability of complete genomic sequences for many organisms today, including *Homo sapiens*, it has become clear that there is a need for data mining techniques to extract the information in them, *e.g.*, gene prediction programs. Of these, the most successful ones are those based on the comparison of known protein or protein-derived information, or those that use expressed sequence tags (ESTs) to predict gene location and structure.

One such algorithm is GeneWise. It bases its exon prediction on the use of Hidden Markov Models (HMMs) of proteins to be compared against a genomic sequence, so that the translation of the sequence will match the model in a similar way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5 (1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3): 405-20 (1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed.

Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR database (Horn *et al.*, *Nucleic Acids Res.* 26(1): 275-9 (1998)), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11): 444-6 (1997)), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349 (2001)), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2 (1999)), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305 (2000)) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48 (2000)). When none is available, or the sequences included in some groups are too disrinatly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680 (1994)) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8(1999)). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally

suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October 2000 Fixed Release (with its subsequent corrections) and the April 2001 Fixed Release (Tables I and II, respectively) of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1):44-47 (2000)) using BLAST (Altschul *et al.*. *Nucleic Acids Res.* 25:3389-3402 (1997)).

Over 80% of the sequences were 90% or more identical to an existing human RefSeq entry and/or mRNAs from GenBank. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to complete the

match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10):1631-42 (2000)).

Of the remaining sequences, over 50% have a match over 90% identical in the public domain protein databases, and the differences between those sequences in the databases and the potential translations is basically the same as the differences between the DNA sequences and the RefSeq entries.

The full sequences of the protein kinase genes and splice variants are shown in the sequence listing. The amino acids encoded by these nucleic acids are also set forth in the sequence listing.

A number of the genes were linked with markers known to be associated with human diseases genes. These are shown in Table IV. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE genetics) are also located in the same consensus using ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction from the marker. The output is the name of the peak marker and its distance to the HMM gene.

NUCLEIC ACIDS OF THE INVENTION

Accordingly, the invention pertains to isolated nucleic acid molecules comprising human protein kinase genes. The term, "protein kinase", as used herein, refers to an isolated nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes protein kinase polypeptide (*e.g.*, a polypeptide selected from the group consisting of SEQ ID NOs: 1-80 (even numbers)). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA

transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a protein kinase polypeptide (*e.g.*, a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers)), or another splicing variant of a protein kinase polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a protein kinase polypeptide of the present invention are also the subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a protein kinase polypeptide. Such variants can be naturally-occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a protein kinase polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a protein kinase gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a protein kinase.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%,

85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of Ç17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1):11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12 , and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and

Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs: 1-80 (even numbers), or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500 (1991).

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs: 1-80 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the

contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967 (1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a

polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs: 1-80 (odd numbers) and/or the complement of one or more of SEQ ID NOs: 1-80 (odd numbers), and/or a portion of one or more of SEQ ID NOs: 1-80 (odd numbers), or the complement of one or more of SEQ ID NOs: 1-80 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs: 1-80 (even numbers), or encoding a portion of one or more of SEQ ID NOs: 1-80 (even numbers), and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as

polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs: 1-80 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid

molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous protein kinase gene, or an

exogenous nucleic acid encoding a protein kinase polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by protein kinases ("protein kinase polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*,

other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-80 (odd numbers), or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also

encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs: 1-80 (odd numbers), or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or 95% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or more of SEQ ID NOs: 1-80 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs: 1-80 (odd numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences

(*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol. 224*:899-904 (1992); de Vos *et al.*, *Science 255*:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs: 1-80 (odd numbers), or a complement of such a nucleic acid (*e.g.*, SEQ ID NOs: 1-80 (odd numbers), or other variants). However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be

increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition, 8*:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry, 270*,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be

used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies that bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites are also provided. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs: 1-80 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs: 1-80 (odd numbers), or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and $F(ab')_2$ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4:72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96) or trioma technique. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *Surf*ZAP™

Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection of the antibody can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, bata-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a protein kinase gene or gene product in an individual. Diagnostic assays can be designed for assessing protein kinase gene expression, or for assessing activity of protein kinase polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a protein kinase, or a defect in a protein kinase. The invention also provides for prognostic (or predictive) assays for determining whether an individual is susceptible to a disease of condition associated with a protein kinase. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a protein kinase. Another aspect of the invention pertains to assays for monitoring the influence of agents (*e.g.*, drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a protein kinase, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with a protein kinase.

In one embodiment of the invention, susceptibility to a disease or condition associated with a protein kinase is diagnosed by detecting a polymorphism in a protein kinase as described herein. The polymorphism can be a mutation in a protein kinase, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding

sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a protein kinase gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a protein kinase can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a protein kinase gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the gene. A protein kinase gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a susceptibility to a disease or condition associated with a protein kinase, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a protein kinase (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a protein kinase is present, and/or to determine which splicing variant(s) encoded by the protein kinase is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a protein kinase or contains a nucleic acid encoding a particular splicing variant of a protein kinase. The probe can be any of

the nucleic acid molecules described above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose susceptibility to a disease or condition associated with a protein kinase, the test sample containing a protein kinase is contacted with at least one nucleic acid probe to form the hybridization sample. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs: 1-80 (odd numbers). Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a protein kinase. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the protein kinase in the test sample, then the protein kinase has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the protein kinase, or of the presence of a particular splicing variant encoding the protein kinase and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a susceptibility to a disease or condition

associated with a protein kinase. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a protein kinase, or of the presence of a particular splicing variant encoded by a protein kinase, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. Hybridization of the PNA probe to a protein kinase is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a protein kinase (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the protein kinase, and therefore indicates the presence or absence of this susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

Sequence analysis can also be used to detect specific polymorphisms in a protein kinase. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a protein kinase, or a fragment of the gene, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA,

is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene, cDNA (*e.g.*, one or more of SEQ ID NOs: 1-80 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs: 1-80 (odd numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the protein kinase indicates that the individual has a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a protein kinase, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a protein kinase, and that contains a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a protein kinase can be prepared, using standard methods (see *Current Protocols in Molecular Biology*, *supra*). To identify polymorphisms in the gene that are associated with a susceptibility to a susceptibility to a disease or condition associated with a protein kinase, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a protein kinase, and its flanking sequences. The DNA containing the amplified protein kinase (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology*, *supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified protein kinase is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the protein kinase, and is therefore indicative of a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a protein kinase. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface

of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261; the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately

from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein.

Other methods of nucleic acid analysis can be used to detect polymorphisms in a protein kinase or variants encoding by a protein kinase. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.* U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a protein kinase can also be made by examining expression and/or composition of a protein kinase polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a protein kinase, or for the presence of a particular variant encoded by a protein kinase. An alteration in expression of a polypeptide encoded by a protein kinase can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a protein kinase is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant protein kinase polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of susceptibility to a disease or condition associated with a protein kinase is made by detecting a particular splicing variant encoded by that protein kinase, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a protein kinase in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a protein kinase. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. Various means of examining expression or composition of the polypeptide encoded by a protein kinase can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant protein kinase, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a protein kinase, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant protein kinase, or the absence in a test sample of a particular splicing variant or of a

polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase, as is the presence (or absence) of particular splicing variants encoded by the protein kinase gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a protein kinase in a test sample is compared with the level or amount of the polypeptide encoded by the protein kinase in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the protein kinase, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that protein kinase. Alternatively, the composition of the polypeptide encoded by a protein kinase in a test sample is compared with the composition of the polypeptide encoded by the protein kinase in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that protein kinase. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a susceptibility to a disease or condition associated with that protein kinase.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as decribed herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) protein kinase polypeptide, means for amplification of nucleic acids comprising a protein kinase, or means for analyzing the nucleic acid sequence of a protein kinase or for analyzing the amino acid sequence of a protein kinase polypeptide, etc.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs: 1-80 (odd numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a protein kinase nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, protein kinase binding

agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with protein kinase binding agents (*e.g.*, receptors or other binding agents); or which alter posttranslational processing of the protein kinase polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a protein kinase polypeptide, a cell, cell lysate, or solution containing or expressing a protein kinase polypeptide (*e.g.*, one of SEQ ID NOs: 1-80 (odd numbers), or another splicing variant encoded by a protein kinase), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of protein kinase activity is assessed (*e.g.*, the level (amount) of protein kinase activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the protein kinase polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a protein kinase polypeptide. An increase in the level of protein kinase activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) protein kinase activity. Similarly, a decrease in the level of protein kinase activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) protein

kinase activity. In another embodiment, the level of activity of a protein kinase polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters protein kinase activity.

The present invention also relates to an assay for identifying agents which alter the expression of a protein kinase gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a protein kinase polypeptide (*e.g.*, a protein kinase gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of protein kinase expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the protein kinase expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of a protein kinase. Enhancement of protein kinase expression indicates that the agent is an agonist of protein kinase activity. Similarly, inhibition of protein kinase expression indicates that the agent is an antagonist of protein kinase activity. In another embodiment, the level and/or pattern of protein kinase polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters protein kinase expression.

In another embodiment of the invention, agents which alter the expression of a protein kinase gene or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the protein kinase gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the protein kinase, as indicated by its ability to alter expression of a gene that is operably linked to the protein kinase gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of protein kinase activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of protein kinase activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters f expression.

Agents which alter the amounts of different splicing variants encoded by a protein kinase (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a protein kinase binding agent. For example, a cell that expresses a compound that interacts with a protein kinase (herein referred to as a "protein kinase binding agent", which can be a polypeptide or other molecule that interacts with a protein kinase, such as a receptor) is contacted with a protein kinase in the presence of a test agent, and the ability of the test agent to alter the interaction between the protein kinase and the protein kinase binding agent is determined. Alternatively, a cell lysate or a solution containing the protein kinase binding agent, can be used. An agent which binds to the protein kinase or the protein kinase binding agent can alter the interaction by interfering with, or enhancing the ability of the protein kinase to bind to, associate with, or otherwise interact with the protein kinase binding agent. Determining the

ability of the test agent to bind to a protein kinase or a protein kinase binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I, ^{35}S, ^{14}C or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a protein kinase or a protein kinase binding agent without the labeling of either the test agent, protein kinase, or the protein kinase binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a protein kinase or antagonists for studying a susceptibility to a disease or condition associated with a protein kinase. Drugs could be designed to regulate protein kinase activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more protein kinase polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more protein kinase polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the

invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a protein kinase polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the protein kinase polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a protein kinase polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the protein kinase polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a protein kinase polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the protein kinase, the protein kinase binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a protein kinase or a protein kinase binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a protein kinase is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test

agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a protein kinase, or to alter expression of a protein kinase, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs: 1-80 (even numbers)); and/or comprising other splicing variants encoded by a protein kinase; and/or an agent that alters (*e.g.*, enhances or inhibits) protein kinase gene expression or protein kinase polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a protein kinase receptor), an agent that alters protein kinase gene expression, or a protein kinase binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters protein kinase polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a

pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl pyrollidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devises ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be

dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with a protein kinase, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a

notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a protein kinase, using a protein kinase therapeutic agent. A "protein kinase therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) protein kinase polypeptide activity and/or protein kinase gene expression, as described herein (*e.g.*, a protein kinase agonist or antagonist). Protein kinase therapeutic agents can alter protein kinase polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional protein kinase polypeptide or by upregulating the transcription or translation of the protein kinase gene; by altering posttranslational processing of the protein kinase polypeptide; by altering transcription of protein kinase splicing variants; or by interfering with protein kinase polypeptide activity (*e.g.*, by binding to a protein kinase polypeptide), or by downregulating the transcription or translation of a protein kinase gene. Representative protein kinase therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a protein kinase polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs: 1-80 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs: 1-80 (odd numbers), or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs: 1-80 (even numbers), and/or other splicing variants encoded by a protein kinase, or fragments or derivatives thereof);

other polypeptides (*e.g.*, protein kinase receptors); protein kinase binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant protein kinase polypeptide, or an antibody to a non-mutant protein kinase polypeptide, or an antibody to a particular splicing variant encoded by a protein kinase, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) protein kinase gene expression or polypeptide activity, or that regulate transcription of protein kinase splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed.

More than one protein kinase therapeutic agent can be used concurrently, if desired.

A protein kinase therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a protein kinase. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a protein kinase polypeptide in an individual. For example, a protein kinase therapeutic agent can be administered in order to upregulate or increase the expression or availability of the protein kinase gene or of specific splicing variants of protein kinase, or, conversely, to downregulate or decrease the expression or availability of the protein kinase gene or specific splicing variants of the protein kinase. Upregulation or increasing expression or availability of a native protein kinase gene or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native protein kinase gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The protein kinase therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the

disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a protein kinase polypeptide, such as one of SEQ ID NOs: 1-80 (even numbers), or a complement thereof; or another nucleic acid that encodes a protein kinase polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs: 1-80 (odd numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a protein kinase or a cDNA encoding a protein kinase polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native protein kinase polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native protein kinase expression and activity, or have mutant protein kinase expression and activity, or have expression of a disease-associated protein kinase splicing variant, can be engineered to express the protein kinase polypeptide or an active fragment of the protein kinase polypeptide (or a different variant of the protein kinase polypeptide). In a preferred embodiment, nucleic acid encoding a protein kinase polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (*e.g.*, microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which

specifically hybridizes to the mRNA and/or genomic DNA of a protein kinase is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the protein kinase polypeptide, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the protein kinase polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the protein kinase. In one embodiment, the oligonucleotide probes are modified oligonucleotides which are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the protein kinase. The antisense oligonucleotides bind to protein kinase mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as

the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, Pharm. Res. 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells which express protein kinase *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous protein kinase transcripts and thereby prevent translation of the protein kinase mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively

infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous protein kinase expression can also be reduced by inactivating or "knocking out" protein kinase or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a mutant, non-functional protein kinase (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous protein kinase (either the coding regions or regulatory regions of protein kinase) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the protein kinase *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the protein kinase. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-mutant protein kinases can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional protein kinase, *e.g.*, a gene having one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant protein kinase in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a protein kinase polypeptide variant that differs from that present in the cell.

Alternatively, endogenous protein kinase expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a protein kinase (*i.e.*, the protein kinase promoter and/or enhancers) to form triple helical structures that prevent transcription of the protein kinase in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the protein kinase proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a protein kinase mRNA or gene sequence) can be used to investigate the role of one or protein kinase in developmental events, as well as the

normal cellular function of the protein kinases in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other protein kinase therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to a disease or condition associated with a protein kinase. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant protein kinase polypeptide in conjunction with antisense therapy targeting mutant protein kinase mRNA; administration of a first splicing variant encoded by a protein kinase in conjunction with antisense therapy targeting a second splicing encoded by a protein kinase) can also be used.

The teachings of all publications cited herein are incorporated herein by reference in their entirety.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

Table I

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MOOSE03177 ctg16439 524311..524473, 539059..539119, 569811..569849,
571874..571890, 576704..576824, 576955..577078, 578035..578097,
578405..578505, 578693..578807, 579677..579712

LETYVKLDKLGEGTYATVFKGRSKLTENLVALKEIRLEHEEGAPCTAI
REVSLLKNLKHANIVTLHDLIHTDRSLTLVFEYLVRDSDLKQYLDHCGNLM
SMHNVKIFMFQLLRGLAYCHHRKILHRELKPQNLLINERGELKLADFGLAR
AKSVPTKTYSNEVVTLWYRPPDVLLGSTEYSTPIDMWSCGCIRCCMFEELK
TAQTEYLNGNGVPEQLDSSSWKSMQQMPGIKKEALKREKEKSTKLNTLECT
HFSPALRRCVQCIAQSFLQTRKSMFVEH **(SEQ ID NO: 10)**

ctggaaacatacgtgaaactggacaaactgggagagggcacctatgccacagtcttcaaagggcgcagcaaa
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actgaaaagggaaaaagaaaaatccacaaaactgaacactctggaatgcacacatttcagcccagctctccgtagatgt
gtgcagtgcattgcacaaagctttctgcagactagaaaatccatgtttgtggaacat **(SEQ ID NO: 9)**

MOOSE03219 ctg17937 2644450..2644580, 2645668..2645883,
2649169..2649358, 2649544..2649660, 2649923..2650037, 2650422..2650553,
2650704..2650813, 2650917..2651030

MAAAAAQGGGGGEPRRTEGVGPGVPGEVEMVKGQPFDVGPRYTQPQ
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IRDILRASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILRGL
KYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHDHTGFLTEYVAT
RWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGI
LGSPSQEDLNCIINMKARNYLQSLPSKTKVAWAKLFPKSDSKALDLLDRML
TFNPNKRITVEEALAHPYLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELI
FQETARFQPGVLE **(SEQ ID NO: 12)**

atggcggcggcggcggctcaggggggcgggggcggggagccccgtagaaccgaggggggtcggcccgg
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cacgcttccagcccggagtgctggag **(SEQ ID NO: 11)**

MOOSE03288 ctg17685 34737..34809, 70525..70657, 76156..76460,
79186..79511, 84816..85274

MSTIQSETDCYDIIEVLGKGTFGEVAKGWRRSTGEMVAIKILKNDAYR
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ENNFAPLPARHIRTVTLQVLTALARLKELAIIHADLKPENIMLVDQTRCPFRV
IDFGSASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELH
LGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHHFFKRNPHPDAAN
PWQLNRLTFPDREALAEHADLKSMVELIKRMLTWESHERISPSAALRHPFVS
MQQLRSAHETTHYYQLSLRSYRLSLQVEGKPPTPVVAAEDGTPYYCLAEEK
EAAAPHPVSSPCLLPPQIPHPAPLPQASCPQPQYSEPSLFFCCFFETEQTAMNI
LVRVSWCVQQATSHRFQD **(SEQ ID NO: 14)**

atgtccaccatccagtcggagactgactgctacgacatcatcgaggtcttgggcaaggggaccttcggggagg
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caacaagccacatctcatcgattccaagac **(SEQ ID NO: 13)**

MOOSE03296 ctg15131 27531456..27531520, 27535488..27535536,
27538082..27538115, 27567396..27567455, 27575039..27575093,
27575966..27576031, 27578952..27579024, 27579170..27579278,
27579676..27579759, 27580203..27580297, 27580938..27581060,
27585744..27585827, 27586074..27586120, 27604172..27604247,
27606557..27606605, 27610733..27610808, 27611170..27611264,

27613040..27613182

HCATLEQWPSSYKTRGQRRGIRTKRMKLKCSQHKKMINVDKK
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GGELFEDIVAREYYSEADASHCIHQILESVNHIHQHDIVHRDLKPENL
LLASKCKGAAVKLADFGLAIEVQGEQQAWFGKGFAGTPGYLSPEVL
RKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYD
FPSPEWDTVTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVA
SMMHRQETVECLRKFNARRKLKGAILTTMLVSRNFSGIRKGNLHLLS
QEPQTTVVHNATDGIKGSTESCNTTTEDEDLKVRKQEIIKITEQLIEAI
NNGDFEAYTKICDPGLTSFEPEALGNLVEGMDFHKFYFENLLSKNSK
PIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQGRPRTSQS **(SEQ ID NO: 16)**

cattgtgccacactggaacagtggccctctagctacaagacaagaggtcagagaagaggcattcga
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agtca **(SEQ ID NO: 15)**

MOOSE03301 ctg15131 20101431..20101501, 20107338..20107405, 20116288..20116347, 20168182..20168236, 20169109..20169174, 20172096..20172168, 20172314..20172422, 20172820..20172903, 20173347..20173441, 20174082..20174204, 20178888..20178971, 20179218..20179264, 20180963..20181101, 20185191..20185223

SLTLLSQEEQLVLYRFSRGAFWKYLERREKIETKKIFKCKVKLERKYH
QKLEREARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYY
SEADASHCIHQILESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGL
AIEVQGEQQAWFGKGFAGTPGYLSPEVLRKDPYGKPVDIWACGVILYILLV
GYPPFWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAKNLINQMLTINPAKR
ITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKLKGAILTTMLV
SRNFSGMTESVRKLLQKEVSMDAIKKEGHLCVSLGLFFELTSNRRCGLSWT
LAEAHRRERTGES **(SEQ ID NO: 18)**

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gcagaaagaggtgtctatggatgcaatcaagaaggaagggcacctgtgtgtttctctagggctgttttttgagttgacctcc
aataggagatgtggcttatcctggactctagcagaagctcataggagagagcgtactggagaaagc **(SEQ ID NO: 17)**

MOOSE03304 ctg16704 2286265..2286402, 2292680..2292937, 2310584..2311273

FDPRVTAKYDIKALIGRGSFSRVVRVEHRATRQPYAIKMIETKYREGR
EVCESELRVLRRVRHANIIQLVEVFETQERVYMVMELATGGELFDRIIAKGS
FTERDATRVLQMVLDGVRYLHALGITHRDLKPENLLYYHPGTDSKIIITDFG
LASARKKGDDCLMKTTCGTPEYIAPEVLVRKPYTNSVDMWALGVIAYILLS
GTMPFEDDNRTRLYRQILRGKYSYSGEPWPSVSNLAKDFIDRLLTVDPGAR
MTALQALRHPWVVSMAASSSMKNLHRSISQNLLKRASSRCQSTKSAQSTRS
SRSTRSNKSRRQGPSKGLLEKRVISPHVSPVTLISLENLESQAQHVQTEDELH
VSSA **(SEQ ID NO:20)**

tttgacccacgtgttacagctaagtatgacatcaaggccctaattggccgaggcagcttcagccgagtggtacgt
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MOOSE03306 ctg19011 264101..264248, 274458..274708, 289937..290629

TCLVFLPNRYDIKALIGTGSFSRVVRVEQKTTKKPFAIKVMETREREGR
EACVSELSVLRRVSHRYIVQLMEIFETEDQVYMVMELATGGELFDRLIAQGS
FTERDAVRILQMVADGIRYLHALQITHRNLKPENLLYYHPGEESKILITDFGL
AYSGKKSGDWTMKTLCGTPEYIAPEVLLRKPYTSAVDMWALGVITYALLS
GFLPFDDESQTRLYRKILKGKYNYTGEPWPSISHLAKDFIDKLLILEAGHRMS
AGQALDHPWVITMAAGSSMKNLQRAISRNLMQRASPHSQSPGSAQSSKSH

YSHKSRHIVKSKGKANKSHRISLLFLADFFHKKIKNIIVVYIPAYNLSEEKNG
KMES **(SEQ ID NO: 22)**

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acaaaagccacagaatatctttgttattcctagcagatttttttcacaagaagattaagaatataattgttgtttatatcccagcc
tataatttatcagaagagaaaaacgggaaaatggaatct **(SEQ ID NO: 21)**

MOOSE03309 ctg13286 2403676..2403725, 2408633..2408761,
2411864..2411938, 2414186..2414324, 2414970..2415093, 2416508..2416583,
2417630..2417742, 2418501..2418579, 2418849..2418879, 2420557..2420616,
2429097..2429163, 2431840..2432054

QTTNIRKTFIFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDS
SLENEIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILERGVYT
EKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPEENSKIMITDFGLSK
MEQNGIMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVITYILLCGYPPFYE
ETESKLFEKIKEGYYEFESPFWDDISESAKDFICHLLEKDPNERYTCEKALSH
PWVQCSVLVIQEKPLDPAPLRSPSPRHLSWTTVGEGRRSRERKNIRKGKRQE
KVYGGVKEATQSPSITNPTPHLGNQQPDISMTTKHQKQPDISMRAKDQKLV
SLATTELTVSSTRVGMAGGVGFS **(SEQ ID NO: 24)**

cagaccaccaacatccggaaaaccttcatttttatggaagtgctgggatcaggagctttctcagaagttttcctggt
gaagcaaagactgactgggaagctctttgctctgaagtgcatcaagaagtcacctgccttccgggacagcagcctggag
aatgagattgctgtgttgaaaaagatcaagcatgaaaacattgtgaccctggaggacatctatgagagcaccacccacta
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agcaccagaaacagccagacatctccatgagagctaaggaccagaaactggtttccttggcaaccactgagctcacagt
gagcagtacaagggtcgggatggctgggggagtggggttctca **(SEQ ID NO: 23)**

MOOSE03312 ctg13538 6574090..6574201, 6574516..6574611,
6592507..6592547, 6603133..6603342, 6605378..6605458, 6606064..6606160,
6613288..6613365, 6613889..6614022, 6620936..6621082, 6621308..6621427,

6629205..6629262, 6632097..6632182

ESSTLLEKYKIGKVIGDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKE
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TERDGSAMVYNLANALRYLHGLSIVHRDIKPENLLVCEYPDGTKSLKLGDF
GLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDIWAAGVITYILLCGFPPF
RSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQVNVEARCTAG
QILSHPWVSPMQPWAGPAHREQVEASQPPRQGPWFSPHTPRSREQGWSGLS
QSWSWLQQLSNQTCQGDGRLSFTSGPPTLSLQKKKIFFSKFMAATNHVAVQ
HWKCALSKLRHAINVKHTRFQSHEDILGEVLPNAFNLYIQYISIIATFLKREG
ERKREK **(SEQ ID NO: 26)**

gaatcatcaactcttcttgagaaatacaaaattggaaaggtcattggtgatggcaattttgcagtagtcaaagagtg
tatagacaggtccactggaaaggagtttgccctaaagattatagacaaagccaaatgttgtggaaaggaacacctgattg
agaatgaagtgtcaatactgcgccgagtgaaacatcccaatatcattatgctggtcgaggagatggaaacagcaactga
gctctttctggtgatggaattggtcaaaggtggagatctctttgatgcaattacttcgtcgaccaagtacactgagagagatg
gcagtgccatggtgtacaacttagccaatgccctcaggtatctccatggcctcagcatcgtgcacagagacatcaaacca
gagaatctcttggtgtgtgaatatcctgatggaaccaagtctttgaaactgggagactttgggcttgcgactgtggtagaag
gccctttatacacagtctgtggcacacccacttatgtggctccagaaatcattgctgaaactggctatggcctgaaggtgg
acatttgggcagctggtgtgatcacatacatacttctctgtggattcccaccattccgaagtgagaacaatctccaggaaga
tctcttcgaccagatcttggctgggaagctggagtttccggccccctactgggataacatcacggactctgccaaggaatt
aatcagtcaaatgcttcaggtaaatgttgaagctcggtgtaccgcgggacaaatcctgagtcacccctgggtgtcaccaat
gcaaccctgggcgggaaggccagctcaccgtgagcaggtagaagccagccagccacccaggcagggaccttggttc
tccccacacactcccaggagcagggaacaggggtggagtggcctttcccagagctggagttggctgcagcagctttcg
aatcagacctgccaaggtgatgggcgtctgagtttcacatctgggccccccaccctgtctctacagaaaaaaaaaattttt
tttcaaaattcatggcagccactaaccacgtggctgttcaacactggaaatgtgccctgtccaaactgagacatgctataaa
tgtaaagcacaccagatttcaaagccatgaagatattctgggggaagttttgccaaatgccttcaatttatatattcaatacat
ttctatcatagcaacctttctgaaaagagagggtgagaggaagagagagaaa **(SEQ ID NO: 25)**

MOOSE03313 ctg595 6983799..6984235, 7002305..7003166

DAAVLKRRGYLLGINLGEGSYAKVKSAYSERLKFNVAIKIIDRKKAPA
DFLEKFLPREIEILAMLNHCSIIKTYEIFETSHGKVYIVMELAVQGDLLELIKT
RGALHEDEARKKFHQLSLAIKYCHDLDVVHRDLKCDNLLLDKDFNIKLSDF
SFSKRCLRDDSGRMALSKTFCGSPAYAAPEVLQGIPYQPKVYDIWSLGVILY
IMVCGSMPYDDSNIKKMLRIQKEHRVNFPRSKHLTGECKDLIYHMLQPDVN
RRLHIDEILSHCWMQPKARGSPSVAINKEGENKTTKMGRNQSRKAENSKNQ
SAFSPPKDHSSSPAMEQSWTENDFDKLTEVGFRRSVITNFSKLKEDVRTHHK
EAKSLEKRLDQWLNRINSVEETLNDLMELKTMARELRDACTRFNSQFDQVE
ERVSVIEDQINEIKQEEKVREKS **(SEQ ID NO: 28)**

gacgctgctgtcctcaagcgacgaggctacctcctggggataaatttaggagagggctcctatgcaaaagtaaa
atctgcttactctgagcgcctgaagttcaatgtggcgatcaagatcatcgaccgcaagaaggcccccgcagacttcttgg
agaaattccttccccgggaaattgagattctggccatgttaaaccactgctccatcattaagacctacgagatctttgagac
atcacatggcaaggtctacatcgtcatggagctcgcagtccagggcgacctcctcgagttaatcaaaacccggggagcc
ctgcatgaggacgaagctcgcaagaagttccaccagctttccttggccatcaagtactgccacgacctggacgtcgtcca
ccgggacctcaagtgtgacaaccttctccttgacaaggacttcaacatcaagctgtccgacttcagcttctccaagcgctg
cctgcgggatgacagtggtcgaatggccttaagcaagaccttctgtgggtcaccagcgtatgcggccccagaggtgctg
cagggcattccctaccagcccaaggtgtacgacatctggagcctaggcgtgatcctctacatcatggtctgcggctccat
gccctacgacgactccaacatcaagaagatgctgcgtatccagaaggagcaccgcgtcaacttcccacgctccaagca
cctgacaggcgagtgcaaggacctcatctaccacatgctgcagcccgacgtcaaccggcggctccacatcgacgagat
cctcagccactgctggatgcagcccaaggcacggggatctccctctgtggccatcaacaaggagggggagaataaaa

ccacaaagatggggagaaaccagagcagaaaagctgaaaattctaaaaaccagagtgccttttctcctccaaaggatca
cagctcctcgccagcaatggaacaaagctggacggagaatgactttgacaagctgacagaagtaggcttcagaaggtc
ggtaataacaaacttctccaagctaaaggaggatgttcgaacccatcacaaggaagctaaaagccttgaaaaaagattag
accaatggctaaatagaataaacagtgtagaggagaccttaaatgacctgatggagctgaaaaccatggcacgagaact
acgtgacgcatgcacaagatttaatagccaattcgatcaagtggaagaaagggtatcagtgattgaagatcaaattaatga
aataaagcaagaagagaaagttagagaaaaaagc **(SEQ ID NO: 27)**

MOOSE03314 ctg595 6468110..6468440, 6516667..6517550

DAAVLKRRGYLLGINLGEGSYAKVKSAYSERLKFNVAIKIIDRKKAPA
DFLEKFLPREIEILAMLNHCSIIKTYEIFETSHGKVYIVMELAVQGDLLELIKT
RGALHEDEARKKFHQLSLAIKYCHDLDVVHRDLKCDNLLLDKDFNIKLSDF
SFSKRCLRDDSGRMALSKTFCGSPAYAAPEVLQGIPYQPKVYDIWSLGVILY
IMVCGSMPYDDSNIKKMLRIQKEHRVNFPRSKHLTGECKDLIYHMLQPDVN
RRLHIDEILSHCWMQPKARGSPSVAINKEGESSRGTEPLTEVITNSLSDHSGI
KLKLTIKKLTQNCTTSWNLNNNVLLNDYWVVNNEIKAEIIKFFETNENKDTSY
QNLWTLAKAVFRGKFIELNAHKRKQERSKIDTLTSQLKELESRA **(SEQ ID NO: 30)**

gacgctgctgtcctcaagcgacgaggctacctcctggggataaatttaggagagggctcctatgcaaaagtaaa
atctgcttactctgagcgcctgaagttcaatgtggcgatcaagatcatcgaccgcaagaaggcccccgcagacttcttgg
agaaattccttccccgggaaattgagattctggccatgttaaaccactgctccatcattaagacctacgagatctttgagac
atcacatggcaaggtctacatcgtcatggagctcgcggtccagggcgacctcctcgagttaatcaaaacccggggagcc
ctgcatgaggacgaagctcgcaagaagttccaccagctttccttggccatcaagtactgccacgacctggacgtcgtcca
ccgggacctcaagtgtgacaaccttctccttgacaaggacttcaacatcaagctgtccgacttcagcttctccaagcgctg
cctgcgggatgacagtggtcgaatggccttaagcaagaccttctgtgggtcaccagcgtatgcggccccagaggtgctg
cagggcattccctaccagcccaaggtgtacgacatctggagcctaggcgtgatcctctacatcatggtctgcggctccat
gccctacgacgactccaacatcaagaagatgctgcgtatccagaaggagcaccgcgtcaacttcccacgctccaagca
cctgacaggcgagtgcaaggacctcatctaccacatgctgcagcccgacgtcaaccggcggctccacatcgacgagat
cctcagccactgctggatgcagcccaaggcacggggatctccctctgtggccatcaacaaggaggggagagttccc
ggggaactgaacccttaacagaagtcataacaaacagtctctcagaccacagtggaatcaaattaaaactcacgattaag
aaactcactcaaaactgcacaacctcatggaacctgaacaacaacgtgctcctgaatgactactgggtaaataacgaaatt
aaggcagaaataattaagttctttgaaaccaatgagaacaaagacacatcataccagaatctctggacactagctaaagc
agtgtttagagggaaatttatagaactaaatgcccacaagagaaagcaggaaaggtctaaaattgacaccctaacatcac
aattaaaggaactagaaagcagagca **(SEQ ID NO: 29)**

MOOSE03316 ctg22fin3 2266883..2267851, 2269136..2269261

DATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRKKTPT
DFVERFLPREMDILATVNHGSIIKTYEIFETSDGRIYIIMELGVQGDLLEFIKCQ
GALHEDVARKMFRQLSSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFG
FSKRCLRDSNGRIILSKTFCGSAAYAAPEVLQSIPYQPKVYDIWSLGVILYIM
VCGSMPYDDSDIRKMLRIQKEHRVDFPRSKNLTCECKDLIYRMLQPDVSQR
LHIDEILSHSWLQPPKPKATSSASFKREGEGKYRAECKLDTKTGLRPDHRPD
HKLGAKTQHRLLVGNLRVQLPRAPFLLHIPPEKQKALQDVSSTQNTGSECR
RKQR **(SEQ ID NO: 32)**

gatgccacagtcctaaggaagaagggttacatcgtaggcatcaatcttggcaagggttcctacgcaaaagtcaa
atctgcctactctgagcgcctcaagttcaatgtggctgtcaagatcatcgaccgcaagaaaacacctactgactttgtgga
gagattccttcctcgggagatggacatcctggcaactgtcaaccacggctccatcatcaagacttacgagatctttgagac
ctctgacggacggatctacatcatcatggagcttggcgtccagggcgacctcctcgagttcatcaagtgccagggagcc
ctgcatgaggacgtggcacgcaagatgttccgacagctctcctccgccgtcaagtactgccacgacctggacatcgtcc

accgggacctcaagtgcgagaaccttctcctcgacaaggacttcaacatcaagctgtctgactttggcttctccaagcgct
gcctgcgggacagcaatgggcgcatcatcctcagcaagaccttctgcgggtcggcagcatatgcagcccccgaggtg
ctgcagagcatcccctaccagcccaaggtgtatgacatctggagcctgggcgtgatcctgtacatcatggtctgcggctc
catgccctatgacgactccgacatcaggaagatgctgcgtatccagaaggagcaccgtgtggacttcccgcgctccaag
aacctgacctgcgagtgcaaggacctcatctaccgcatgctgcagcccgacgtcagccagcggctccacatcgatgag
atcctcagccactcgtggctgcagccccccaagcccaaagccacgtcttctgcctccttcaagagggaggggagggc
aagtaccgcgctgagtgcaaactggacaccaagacaggcttgaggcccgaccaccggcccgaccacaagcttgga
gccaaaacccagcaccggctgctggtggggaacctaagggtacaacttccaagggctccgtttctccttcatatcccccc
agagaagcagaaagcactgcaggatgtgagctcaactcagaacacaggttccgagtgccgcagaaagcaacgc
(SEQ ID NO: 31)

MOOSE03330 ctg14489 3270126..3270273, 3271022..3271654,
3272933..3272941, 3276338..3276388, 3288738..3288805, 3332756..3332897,
3349729..3349937

SMEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGG
PEEFIQRFLPRELQIVRTLDHKNIIQVYEMLESADGKICLVMELAEGGDVFDC
VLNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALLQGFNLKL
TDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGIPHDSKKGDVWSMGVVL
YVMLCASLPFDDTDIPKMLWQQQKGVSFPTHLSISADCQDLLKRLLEPDMIL
RPSIEEVKQHRWFQTPDLNDLATSASQDTGHRKHPFSARILSQPQSSFSLEIQ
NAELASPAHWGKVQPPQEDLEAQLGSLGGLQKVSSPQGALVSELAMEMQS
YYAKLLGELNEQRKRDFFCDCSIIVEGRIFKAHRNILFANSGYFRALLIHYIQ
DSGRHSTASLD **(SEQ ID NO: 34)**

agcatggaggactttctgctctccaatgggtaccagctgggcaagaccattggggaagggacctactcaaaagt
caaagaagcattttccaaaaaacaccaaagaaaagtggcaattaaagttatagacaagatgggagggccagaagagttt
atccagagattcctccctcgggagctccaaatcgtccgtaccctggaccacaagaacatcatccaggtgtatgagatgct
ggagtctgccgacgggaaaatctgcctggtgatggagctcgctgagggaggggatgtctttgactgcgtgctgaatggg
gggccactgcctgaaagccgggccaaggccctcttccgtcagatggttgaggccatccgctactgccatggctgtggtg
tggcccaccgggacctcaaatgtgagaacgccttgttgcagggcttcaacctgaagctgactgactttggctttgccaag
gtgttgcccaagtcacaccgggagctgagccagaccttctgcggcagtacagcctatgctgcccccgaggtgctgcag
ggcattccccacgatagcaaaaaaggtgatgtctggagcatgggtgtggtcctgtatgtcatgctctgtgccagcctacct
tttgacgacacagacatccccaagatgctgtggcagcagcagaaggggtgtccttccccactcatctgagcatctcgg
ccgattgccaggacctgctcaagaggctcctggaacccgatatgatcctccggccttcaattgaagaagttaagcagcat
cgctggtttcaaactcctgacctcaatgatctggccacctcggcctcccaagatactgggcatagaaagcacccttctctg
ccaggatactcagtcaaccacaatccagcttctcccttgaaattcagaatgctgagctggcttctcctgctcactgggga
aagttcagcctccacaggaggacctggaggctcagctggggtcccttggtgggttgcagaaggtttcgtctcctcagggt
gctctggtgtctgagctggcaatggagatgcaatcctattatgccaagcttttgggggagctgaatgaacagagaaagag
ggacttttttctgtgactgcagcatcattgtggaagggcggatcttcaaggcccacaggaacattttgtttgctaacagcggc
tacttccgagccctgctcattcactatatccaggacagcgggcggcatagcaccgcctccttggac **(SEQ ID NO: 33)**

MOOSE03332 ctg15907 2781758..2781942, 2783326..2783392,
2824027..2824141, 2827236..2827388, 2828296..2828408, 2829233..2829307,
2832037..2832178, 2834312..2834421, 2834490..2834592, 2838446..2838457,
2859043..2859095

KLYKLERSYISKLTLGQLHFGKGRFGQVHKCEETATGLKLAAKIIKTR
GMKDKVQPEEVKNEISVMNQLDHANLIQLYDAFESKNDIVLVMEYVDGGE
LFDRIIDESYNLTELDTILFMKQICEGIRHMHQMYILHLDLKPENILCVNRDA

KQIKIIDFGLARRYKLKVNFGTPEFLAPEVVNYDFVSFPTDMWSVGVIAYML
LSGLSPFLGDNDAETLNNILACRWDLEDEEFQDISEEAKEFISKLLIKEKSWRI
SASEALKHPWLSDHKLHSRLNAQVTTASCSSSFSPRGLRARRGGAGKRLCP
VGRRQERIAQEGMEDRKWITSPHGQLKLKVEKTEKLAGGIVSSQPVNFWKK
MDHKEWEVEEKERRNQE **(SEQ ID NO: 36)**

aagctttacaaattagagagatcgtacattagcaagctaaccctagggcaattacattttggaaaagggcgtttcg
gccaggttcacaagtgtgaggagacggccacaggtctgaagctggcagccaaaatcatcaagaccagaggcatgaag
gacaaggtacagcctgaggaggtgaagaacgagatcagcgtcatgaaccagctggaccacgcgaacctcatccagct
gtacgatgccttcgagtctaagaacgacattgtcctggtcatggagtatgtggatggtggggagctgtttgaccgcatcat
cgatgagagctacaatttgacggagcttgataccatcctgttcatgaagcagatatgtgaggggataaggcacatgcatc
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gccaaggagttcatctctaagcttctgattaaggagaagagttggcgaataagtgcaagcgaagctctcaagcacccctg
gttgtcagaccacaagctccactccagactcaatgcccaggtgaccacggcttcttgctcttcctctttttctcctcggggcc
tgcgggcgcggcgtggcggggcgggaaaacggctctgtcccgtggggcgcaggcaggaacggattgcccaggaag
gtatggaggaccgaaaatggatcaccagccctcatggacaacttaaactaaaggtggaaaagacagaaaagctggcag
ggggaattgtctccagccaacctgtcaacttttggaaaaagatggatcacaaagaatgggaagtggaagagaaggaga
ggagaaaccaagaa **(SEQ ID NO: 35)**

MOOSE03340 ctg16586 599905..599948, 614744..614840, 617090..617199, 617282..617423, 621304..621626, 622188..622340, 622489..622638, 664150..664360

KTKQNKTKQRLYLGLGKFGAVCTCMEKATGLKLAAKVIKKQTPKDK
VEMVLLEIEVMNQLNHRNLIQLYAAIETPHEIVLFMEYIEGGELFERIVDEDY
HLTEVDTMVFVRQICDGILFMHKMRVLHLDLKPENILCVNTTGHLVKIIDFG
LARRYHLGGWGGQDKPLSWQGTGVGWRGHGYRPGAVLSALGLTPRYNPN
EKLKVNFGTPEFLSPEVVNYDQISDKTDMWSMGVITYMLLSGLSPFLGDDD
TETLNNVLSGNWYFDEETFEAVSDEAKDFVSNLIVKDQRARMNAAQCLAH
PWLNNLAEKAKRCNRRLKSQILLKKYLMKRRWKVPLDSGKKERERERKERK
KERKKERKKERKKKEGRKKERKKEKERKKKKERKEGRKEGRKKERKKER
KKERKKERKK **(SEQ ID NO: 38)**

aaaacaaagcaaaacaaaacaaaacaaagactctacctggggcttggcaagtttggggcagtctgtacctgcat
ggagaaagccacaggcctcaagctggcagccaaggtcatcaagaaacagactcccaaagacaaggtagaaatggtgt
tgctggagattgaggtcatgaaccagctgaaccaccgcaatctgatccagctgtatgcagccatcgagactccgcatga
gatcgtcctgttcatggagtacatcgagggcggagagctcttcgagaggattgtggatgaggactaccatctgaccgag
gtggacaccatggtgtttgtcaggcagatctgtgacgggatcctcttcatgcacaagatgagggttttgcacctggacctc
aagccagagaacatcctgtgtgtcaacaccacgggcatttggtgaagatcattgactttggcctggcacggaggtaccac
ctgggtgggtggggagggcaagacaagcctctgagttggcaggggacaggggtggggtggaggggcatgggtat
aggccaggagctgtgctctcagcccttggtctcacccccaggtataaccccaacgagaagctgaaggtgaactttggga
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acctacatgctgctgagcggcctctccccttcctgggagatgatgacacagagaccctaaacaacgttctatctggcaa
ctggtactttgatgaagagacctttgaggccgtatcagacgaggccaaagactttgtctccaacctcatcgtcaaggacca
gagggcccggatgaacgctgcccagtgtctcgcccatccctggctcaacaacctggcggagaaagccaaacgctgta
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gaaagaaagagagagagagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaaaag
gaaggaaggaagaaagaaagaaagaaagagaaagaaagaaagaaaaagaaagaaaggaaggaaggaaggaagg

aaggaaggaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaa **(SEQ ID NO: 37)**

MOOSE03350 ctg17207 1395832..1395980, 1407142..1407320, 1409219..1409316, 1428807..1428839, 1436633..1437389, 1441418..1441440

RRHNPRQCELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRR APPDFVNKFLPRELSILRGVRHPHIVHVFEFIEVCNGKLYIVMEAAATDLLQA VQRNGRIPGVQARDLFAQIAGAVRYLHDHHLVHRDLKCENVLLSPDERRV KLTDFGFGRQAHGYPDLSTTYCGSAAYASPEVLLGIPYDPKKYDVWSMGV VLYVMVTGCMPFDDSDIAGLPRRQKRGVLYPEGLELSERCKALIAELLQFSP SARPSAGQGCLGHPCICQSREVCPDSLRPLHQVPFPPRRRKWSCLPGAAPRL LRQENGMNPGGQSLQGAEIVPLRTPAWATARLRLKKKKKKEKKKKKKKNP VTEKKDTVINATLSPKVAKEHTSQPAPSRPWGRPLVQVLPPPTADKPLMVQ GEVGKRRA **(SEQ ID NO: 40)**

aggagacacaaccccaggcagtgcgaactcggttataagctgggccgcacaattggagagggcagctactcc aaggtgaaggtggccacatccaagaagtacaagggtaccgtggccatcaaggtggtggaccggcggcgagcgcccc cggacttcgtcaacaagttcctgccgcgagagctgtccatcctgcggggcgtgcgacacccgcacatcgtgcacgtctt cgagttcatcgaggtgtgcaacgggaaactgtacatcgtgatggaagcggccgccaccgacctgctgcaagccgtgca gcgcaacgggcgcatccccggagttcaggcgcgcgacctctttgcgcagatcgccggcgccgtgcgctacctgcacg atcatcacctggtgcaccgcgacctcaagtgcgaaaacgtgctgctgagcccggacgagcgccgcgtcaagctcacc gacttcggcttcggccgccaggcccatggctacccagacctgagcaccacctactgcggctcagccgcctacgcgtca cccgaggtgctcctgggcatcccctacgaccccaagaagtacgatgtgtggagcatgggcgtcgtgctctacgtcatgg tcaccgggtgcatgcccttcgacgactcggacatcgccggcctgccccggcgccagaaacgcggcgtgctctatcccg aaggcctcgagctgtccgagcgctgcaaggccctgatcgccgagctgctgcagttcagcccgtccgccaggccctccg cgggccagggctgcctcggccatccctgcatctgtcagtcaagagaggtttgccccgacagcctgcgtcccctgcacca ggtcccattcccacctcggagaaggaaatggagttgtttgccgggagctgccccaaggctgctgaggcaggagaatgg catgaaccccgggggggcagagcctgcagggagccgagatcgtgccactgcgcactccagcctgggcgacagccag actccgtctcaaaaaaaaaaaaaaaaaaagaaaaaaaaaaaaagaaaaagaaaaatcctgtgacagagaaaaaggaca cagttatcaatgctactttgagccccaaagtggccaaggaacacacatcccagcctgccccgtccagaccatggggcag gcctttggtccaagtgctgccccctcccacagcagacaagccactcatggtacaaggggaggtggggaagagaagag ca **(SEQ ID NO: 39)**

MOOSE03368 ctg16775 599558..599733, 624104..624251, 628175..628228, 628324..628429, 629746..629811, 629902..629972, 631287..631343, 636534..636770, 642985..643104, 643578..643677, 645436..645545, 645693..645751, 652218..652288, 652509..652726, 662661..663016, 667436..667769

SLRAAPGPRRPSAASSCTSTWPSCATAPAPAHAPGPGPASVSRTSAHSS RCRASYSSATRSLGARCRNSIASCPEEQPHVGNYRLLRTIGKGNFAKVKLAR HILTGREVAIKIIDKTQLNPSSLQKDPPSHPPSLSSVFLSGHAQLFREVRIMKG LNHPNIVKLFEVIETEKTLYLVMEYASAGEVFDYLVSHGRMKEKEARAKFR QIVSAVHYCHQKNIVHRDLKAENLLLDAEANIKIADFGFSNEFTLGSKLDTF CGSPPYAAPELFQGKKYDGPEVDIWSLGVILYTLVSGSLPFDGHNLKELRER VLRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEEL KPYTEPEEDFGDTKRIEVMVGMGYTREEIKESLTSQKYNEVTATYLLLGRKT ERHHQRNKFQQRHQPQQRAAESHHCTPAWQQNQTLSQKKKKKKEGGPSP APLHPKRSPTSTGEAELKEERLPGRKASCSTAGSGSRGLPPSSPMVSSAHNPN KAEIPERRKDSTSTPECEESKGLGPWPASVPHPDLSVSAHSSGTPRVPPASPS

SHSLAPPSGERSRLARGSTIRSTFHGGQVRDRRAGGGGGGGVQNGPPASPTL
AHEAAPLPAGRPRPTTNLFTKLTSKLTRSCHLPWDQTETAPRLLRFPWSVKL
TSSRPPEALMAALRQATAAARCRCRQPQPFLLACLHGGAGGPEPLSHFEVE
VCQLPRPGLRGVLFRRVAGTALAFRTLVTRISNDLEL **(SEQ ID NO: 42)**

agtttgcgggccgccccgggaccccgacgcccgtcggccgcctcctcctgtaccagcacctggcccagctgc
gccaccgcgccagccccggcgcacgctcccggccccggggcccgccagcgtctcgcgcaccagcgcccacagctcg
cgctgcagggcctcgtacagcagcgccacccgctcactgggtgcccgttgccggaactccatcgcctcctgtcccgag
gagcagccccacgtgggcaactaccgcctgctgaggaccattgggaagggcaactttgccaaagtcaagctggctcg
gcacatcctcactggtcgggaggttgccatcaagattatcgacaaaacccagctgaatcccagcagcctgcagaaggat
ccccccaagccacccaccctcactctcctctgtcttcctttctggccacgcccagctgttccgagaagtccgcatcatgaag
ggcctaaaccaccccaacatcgtgaagctctttgaggtgattgagactgagaagacgctgtacctggtgatggagtacgc
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MOOSE03372 ctg21fin5 107539..107634, 114972..115106, 117564..118777, 132517..132645, 134076..134256, 143434..143531, 152410..152623, 152852..153075, 153628..153751, 153861..153985, 154247..154417, 154592..154655, 158025..158141, 158641..158754, 166928..167047, 174177..174241, 196417..196459

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FSAHSYTSNLGDYDEQALGIMQTLGVDRQRTVESLQNSSYNHFAAIYYLLL

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GGLASRGGGGERGDAPARGRSLGPAWREPRQDPPNCDGMNFGSHRKLRSP
NTPVPIREGQKTHALSHQGYQGRAWAGVLAPEPRIPASSSQLPRERAVSNSQ
QPGLWAEMVAVSCPASPPLRGQGAPLLTLYLETTQPHGLWASSSRCPICPAS
SAWAQSSPQDTVQDAQTPRARGTGSAGIPPPGPTPHRVFCRAWENQAPGQD
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HTHSRDAHHTHQGPPQTHTPGTHTHQGHTHHTHTRDTHHTHQGHTPGTDT
QGMHTHQGRTAHTPGTHTHTRDAHTSGTHKHQGRTPHTPGTHTTHTHTMD
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AHTPSSDTHTPSHTHHTPIRHPHIISHTTHSPDTHTSSHTHHTPIRHPTSSHTHY
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PLPL **(SEQ ID NO: 44)**

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MOOSE03412 ctg13513 7184425..7185657, 7186318..7186470, 7187454..7187616, 7188719..7188850, 7190165..7190307, 7191013..7191144, 7196317..7196463

MVGKLSRRIYLSSARMVTTVPHVFSKLLEMLSVSSSTHFTRMRRRLM
AIADEVEIAEAIQLGVEDTLDGQQDSFLQASVPNNYLETTENSSPECTIHLEK
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PQTQRKFSLQFHRNCPENKDSDKLSPVFTQSRPLPSSNIHRPKPSRPTPGNTS
KQGDPSKNSMTLDLNSSSKCDDSFGCSSNSSNAVIPSDETVFTPVEEKCRLD
VNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPEKAENDDTYKDDVNHN
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VRNTSSEQEEVVEALREEIRMMSHLNHPNIIRMLGATCEKSNYNLFIEWMA
GGSVAHLLSKYGAFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDS
TGQRLRIADFGAAARLASKGTGAGEFQGQLLGTIAFMAPEVLRGQQYGRSC
DVWSVGCAIIEMACAKPPWNAEKHSNHLALIFKIASATTAPSIPSHLSPGLRD
VALRCLELQPQDRPPSRELLKHPVFRTTW **(SEQ ID NO: 46)**

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MOOSE03452 ctg15649 811724..811807, 812519..812659, 812773..812850, 814237..814367, 814923..815172, 818062..818155, 818454..818623, 844037..844171, 849058..849146, 852486..852611, 852628..852835, 868504..868616, 868765..868828, 877314..877424

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HVTIITEPAGPDLGTPFTSRLPPELQVLKDEQAHRLAPKGNQSRILTQAYKR
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SPDPTALKGLRVRESGDDPPLQAPEPPRFPALASRPLLPDSRSKSLKKKIKITY
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QKSPVFCVDHVGSSRSELFLFGHLSFLSFLS **(SEQ ID NO: 48)**

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ttctttcttttctttcc **(SEQ ID NO: 47)**

MOOSE03453 ctg15214 7151184..7151300, 7153202..7153295, 7153383..7153480, 7154683..7154766, 7155983..7156050, 7156143..7156229,

7158906..7158960, 7162484..7162684, 7163180..7163206, 7169239..7169373, 7170472..7170578, 7187302..7187365, 7200868..7200941, 7204145..7204249, 7207958..7208046, 7208619..7208728, 7214615..7214648, 7216785..7216853, 7216976..7216995

MDDYMVLRMIGEGSFGRALLVQHESSNQMFAMKEIRLPKSFSNTQNS RKEAVLLAKMKHPNIVAFKESFEAEGHLYIVMEYCDGGDLMQKIKQQKGK LFPEDMILNWFTQMCLGVNHIHKKRVLHRDIKSKNIFLTQNGKVKLGDFGS ARLLSNPMAFACTYVGTPYYVPPEIWENLPYNNKSDIWSLGCILYELCTLKH PFQANSWKNLILKVCQGCISPLPSHYSYELQFLVKQMFKRNPSHRPSATTLL SRGIVARLVQKCLPPEAICLSRLPKAGGSPEPGKLRRAVSYDRTSALQPGQH SKTLSQKEKNFHPLKCFLQEEEQDRKGSHTDLESINENLVESALRRVNREEK GNQGLEVRVEMTSQQSIKSEEEKLRRQQQRLRGMAAAAAGTATSQRCILGK RLKKVCKKKNQYFSLSDYWMSHTDLGKPNTLDSWDYRRPPPRPANFFVFL VEMGFHHVSQDGLGDKAYSQTCLSQFWYVNSRPIQSANRTSALLANSRNSC QGYQMEKKDHYVALQPGQQSETLSQKKKKKDYVWLELR **(SEQ ID NO: 50)**

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MOOSE03455 ctg15214 6841087..6841115, 6863772..6863842, 6868407..6868463, 6885556..6885770, 6890751..6890831, 6891392..6891423, 6891428..6891526, 6891894..6892061, 6895605..6895665, 6908442..6908654, 6910860..6910914, 6914680..6914766, 6916702..6916772, 6916856..6916939, 6918630..6918785, 6927603..6927668, 6929582..6929668

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QSWQKAKEEQSHALHEGRQESLWELLFTKPSDLLKAAVSHDCATVPQPGIQ
SKTRSQKNKALLTSQTGRRGKGAPHISDDGRPGRDAPHFLDGMAAGQRRSS
LSRLGSQAEGLLTSQTMGGRAETLLTSQTGLRQENCLNLGGGGCSEPRSSGE
RGHPCLVPVFKGNASSFCPFKNKDEVRWVR **(SEQ ID NO: 52)**

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3410294..3410996, 3411423..3411517

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DMDEDGYHHSEQTVTRTENQTLHILTHRWELNNENIWTQGGEHHKRGPVM
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LLLEKIEHDDICNKTLKITDFGLAREWHRTTKMSTAGTYAWMAPEVIKSSLF
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AKLMKECWQQDPHIRPSFALILEQLTAIEGAVMTEMPQESFHSMQDDWKLE
IQQMFDELRTKEKELRSREEELTRAALQQKSQEELLKRREQQLAEREIDVLE
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NLDKRRSLNSSSSSPPSSPTMMPRLRAIQLTSDESNKTWGRNTVFRQEEFED
VKRNFKKKGCTWGPNSIQMKDRTDCKERYAYIDLPLGKDAQRENPAEAES
WEEAASANAATVSIEMTPTNSLSRSPQRKKTESALYGCTVLLASVALGLDL
RELHKAQAAEEPLPKEEKKKREGIFQRASKSRRSASPPTSLPSTCGEASSPPS
LPLSSALGILSTPSFSTKCLLQMDSEDPLVDSAPVTCDSEMLTPDFCPTAPGS
GREPALMPRLDTDCSVSRNLPSSFLQQTCGNVPYCASSKHRPSHHRRTMSD

GNPTPSDQPARAAITECHSMERCSAQTHCPAVPEAGS **(SEQ ID NO: 54)**

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ggaagt **(SEQ ID NO: 53)**

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3124825..3124996, 3125298..3125447, 3125740..3125943, 3126172..3126229,
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3136796..3136971, 3140646..3140759, 3143510..3143640, 3146484..3146556,
3147052..3147114, 3153441..3153478, 3156029..3156051, 3157718..3157767,
3159767..3159858, 3163220..3163354, 3163842..3164061, 3165485..3165583

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MSGRSPALWAAPETLQFGHFSSASDVWSFGIIMWEVMAFGERPYWDMSGQ
DVIKAVEDGFRLPPPRNCPNLLHRLMLDCWQKDPGERPRFSQIHSILSKMVQ
DPEPPKYPSCRLSTAPLTRRPPTPLADRAFSTFPSFGSVGAWLEALDLCRYKD
SFAAAGYGSLEAVAEMTAQDLVSLGISLAEHREALLSGISALQARVLQLQG
QGV **(SEQ ID NO: 56)**

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ggggtg **(SEQ ID NO: 55)**

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1299634..1299694, 1300281..1300444, 1302529..1302597, 1304778..1304876, 1308725..1308852, 1308870..1308971, 1310153..1310182, 1312286..1312408, 1315361..1315590, 1324030..1324058, 1324580..1324606, 1326221..1326279, 1326793..1326866, 1327879..1328563, 1331470..1331534, 1334870..1334952, 1372438..1372478

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MOOSE03639 ctg13657 34913..34950, 82022..82239, 82529..82663, 82800..82929, 83247..83406, 83533..83643, 84139..84368, 84550..84614, 85310..85415, 85597..85759, 85842..85978, 86211..86431, 86507..86548, 86754..86949, 87087..87254, 87654..87892, 90056..90182, 90381..90595, 92425..92569, 92781..92923, 93023..93326, 94887..95438, 99458..99542

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(SEQ ID NO: 59)

Table II

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FELIEQRYVAVKIHQLNKNWRDEKKENYHKHACREYWIHKELDHPRIIKLY
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NKIKPPIIHYDLKPGNILLVNGTVCGERKITELGLSKIMDDDSYNSVGGMELT
SQGAGTYCNLTPESFVVEKEPPKISNKIVVWSVGVIFYQCLSGGKPFGYNQS
QQDILQENTILKAAEEESVLLSQGWQRQKWRRWKGGRRGKHTWYNFPELH
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ISFLSSTFFHWNPTESNSNIKILTL **(SEQ ID NO: 62)**

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MOOSE08757 ctg13715 6930203..6930273, 6930668..6930767, 6932774..6933773, 6951271..6951367, 6954877..6954931

SIVINHISVSVSELTRINKNAKIKTHTHSHLIFNQVDKSKQWGKDTLVN
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SQKVKHPQLLYESKLYTILQGGVGIPHMHWYGQEKDNNVLVMDLLGPSLE
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CNKLFLIDFGLAKKYRDNRTRQHIPYREDKHLIGTVRYASINAHLGIEQSRR
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KQKAAQQAASSSGQGQQAQTQTGKQTEKNKNNLCKTKYRCFCPSISLFHFS
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1638204..1638220, 1644548..1645211, 1647690..1647730, 1649104..1649221

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MOOSE03184 ctg12913 5214792..5214862, 5219393..5219472,
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5254291..5254384, 5261784..5261847, 5286898..5287073

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AEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLP **(SEQ ID NO: 70)**

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aagtcgtgaccctctggtaccggccccctgatgctttgctgggagccactgaatattcctctgagctggacataTGGgg
tgcaggctgcatctttattgaaatgttccagggtcaacctttgtttcctggggtttccaacatccttgaacagctggagaaaat
ctgggaggtgctgggagtccctacagaggatacttggccgggagtctccaagctacctaactacaatccaGGCtgctg
gagaaactctatttttctctcccacttttccaggctgggcagggttcctgaagctgaagacctggcctcccagatgctaaaa
ggctttcccagagaccgcgtctccgcccaggaagcacttgttcatgattatttcagcgccctgccatctcagctgtaccag
cttcct **(SEQ ID NO: 69)**

MOOSE03305 ctg14493 3566412..3566482, 3568893..3569020,
3571689..3571881, 3574372..3574539, 3577889..3578015, 3609346..3609756

IAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYAMKIIDKSRLKG
KEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAIIESVK
FPEPDAALMIMDLCKALVHMHDKSIVHRDLKPENLLRNEDKSTTLKLADFG
LAKHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPPF
RSPERDQDELFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVVDPKKRYTAH
QVLQHPWIETAGKTNTVKRQKQVSPSSEGHFRSQHKRVVEQVSYESIVTES
DQGVCWRWKWGEEGQKDCKGTLGNFGEEGRVHFLELWRRNGEMSPGRE
EGQERVHSRVR **(SEQ ID NO: 72)**

attgccgccaatgtggaaaagcattatgagactggccgggtcattggggatgggaactttgctgtcgtgaagga
gtgcagacaccgcgagaccaggcaggcctatgcgatgaagatcattgacaagtccagactcaagggcaaggaggac
atggtggacagtgagatcttgatcatccagagcctctctcaccccaacatcgtgaaattgcatgaagtctacgaaacagac

atggaaatctacctgatcctggagtacgtgcagggaggagacctttttgacgccatcatagaaagtgtgaagttcccgga
gcccgatgctgccctcatgatcatggacttatgcaaagccctcgtccacatgcacgacaagagcattgtccaccgggac
ctcaagccggaaaacctttgcgaaatgaggacaaatctactaccttgaaattggctgattttggacttgcaaagcatgtgg
tgagacctatatttactgtgtgtgggaccccaacttacgtagctcccgaaattctttctgagaaaggttatggactggaggtg
gacatgtgggctgctggcgtgatcctctatatcctgctgtgtggctttcccccattccgcagccctgagagggaccaggac
gagctctttaacatcatccagctgggccactttgagttcctccccccttactgggacaatatctctgatgctgctaaagatct
ggtgagccggttgctggtggtagaccccaaaaagcgctacacagctcatcaggttcttcagcacccctggatcgaaaca
gctggcaagaccaatacagtgaaacgacagaagcaggtgtcccccagcagcgagggtcacttccggagccagcaca
agagggttgtggagcaggtatcatatgaatctatagtgacagaaagtgatcaggggtttgctggagatggaaatgggg
agaggagggacagaaggattgcaagggaacacttggtaactttggggaagagggacgtgttcattttcttgaattgtgga
gaagaaatggggaaatgagtccaggaagagaggaaggccaagaaagagtgcattcacgtgtgagg **(SEQ ID NO: 71)**

MOOSE03302 ctg15540 6561837..6562051, 6568471..6568519,
6570944..6570985, 6581301..6581378, 6581838..6581921, 6583077..6583199,
6585571..6585665, 6599224..6599307, 6605349..6605451, 6615652..6615724,
6620039..6620102, 6629168..6629314, 6632248..6632285, 6634388..6634550

KGVGRFKDRKYEIIRFHYTKLSLAAVWQGIIGGQNGSGGKWILEESKK
KNDNDLGIGESSRGENLCFIFKSSVRVCHVMEVHAYTGSHYVAQTEFLGSS
DPPALASQNAEVTSLSHHTYLVSPCSNKIYPEYFTGGELFEDIVAREYYSEAD
ASHCIQQILEAVLHCHQMGVVHRDLKPENLLLASKSKGAAVKLADFGLAIE
VQGDQQAWFGFAGTPGYLSPEVLRKDPYGKPVDMWACGVILYILLVGYPP
FWDEDQHRLYQQIKAGAYDFPSPEWDTVTPEAKDLINKMLTINPAKRITASE
ALKHPWICQRSTVASMMHRQETVDCLKKFNARRKLKGAILTTMLATRNFS
GTCIGNSASYPLEPQTTVIHNPDGNKESTESSNTTIEDEDVKEEGITRITNTEK
CLKELMELKTKAQELREECRSLRSRCDQLEERVSVMEDEMNEMKQEGKFR
EKRIKRNEQS **(SEQ ID NO: 74)**

AAAGGTGTTGGAAGATTTAAAGATCGGAAATATGAAATAATCCGA
TTTCATTATACAAAGCTCTCTCTTGCTGCAGTGTGGCAAGGGATTATAGG
AGGGCAGAATGGAAGTGGAGGAAAATGGATATTGGAGGAGTCAAAGAA
AAAAAATGACAATGATTTGGGCATAGGTGAGAGCAGTAGAGGAGAAAA
CTTATGTTTCATCTTCAAAAGCTCAGTAAGAGTGTGCCACGTTATGGAGG
TCCATGCATATACGGGGTCTCACTATGTTGCCCAGACTGAATTCCTGGGC
TCAAGTGATCCTCCTGCCTTGGCCTCCCAAAATGCTGAGGTTACAAGCCT
GAGCCACCACACCTATCTTGTAAGTCCCTGTAGTAATAAAATATATCCTG
AATATTTTACTGGAGGTGAACTGTTTGAAGACATAGTGGCAAGAGAATA
CTACAGTGAAGCTGATGCCAGTCATTGCATTCAGCAGATCCTGGAGGCT
GTGCTACACTGCCATCAGATGGGCGTGGTCCATCGGGACCTGAAGCCTG
AGAATTTGCTTTTAGCTAGCAAATCCAAGGGAGCAGCTGTGAAATTGGC
AGACTTTGGCTTAGCCATAGAAGTTCAAGGGGACCAGCAGGCGTGGTTT
GGTTTTGCTGGCACACCTGGATATCTTTCTCCAGAAGTTTTACGTAAAGA
TCCTTATGGAAAGCCAGTGGATATGTGGGCATGTGGTGTCATTCTCTATA
TTCTACTTGTGGGGTATCCACCCTTCTGGGATGAAGACCAACACAGACTC
TATCAGCAGATCAAGGCTGGAGCTTATGATTTTCCATCACCAGAATGGG
ACACGGTGACTCCTGAAGCCAAAGACCTCATCAATAAAATGCTTACTAT
CAACCCTGCCAAACGCATCACAGCCTCAGAGGCACTGAAGCACCCATGG
ATCTGTCAACGTTCTACTGTTGCTTCCATGATGCACAGACAGGAGACTGT
AGACTGCTTGAAGAAATTTAATGCTAGAAGAAAACTAAAGGGTGCCATC

TTGACAACTATGCTGGCTACAAGGAATTTCTCAGGTACATGCATTGGGA
ACTCTGCTTCTTATCCCTTGGAGCCCCAAACTACTGTAATCCACAACCCT
GATGGAAACAAGGAGTCAACTGAGAGTTCAAATACAACAATTGAGGAT
GAAGATGTGAAAGAAGAAGGTATAACTAGAATAACCAATACAGAGAAG
TGCTTAAAGGAGCTGATGGAGCTGAAAACCAAGGCTCAAGAACTACGTG
AAGAATGCAGAAGCCTCAGGAGCCGATGCGATCAACTGGAAGAAAGGG
TGTCAGTGATGGAAGATGAAATGAATGAAATGAAGCAAGAAGGGAAGT
TTAGAGAAAAAAGAATAAAAAGAAATGAGCAAAGC **(SEQ ID NO: 73)**

MOOSE03376 ctg16439 322580..322679, 326037..326947, 327612..327744, 328601..328720, 330578..330643, 330994..331145, 334118..334238, 344390..344620

MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKH
NLRHRYEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRR
EIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREAR
HFFRQIVSAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKF
LQTFCGSPLYASPEIVNGKPYTGPEVDSWSLGVLLYILVHGTMPFDGHDHKI
LVKQISNGAYREPPKPSAPAFCLPDACGLIRWLLMVNPTRRATLEDVASHW
WVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKV
CSFFKQHAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGK
SNLKLPKGILKKKVSASAEGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQ
RESGYYSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNG
KFSQTALELAAPTTFGSLDELAPPRPLARASRPSGAVSEDSILSSESFDQLDLP
ERLPEPPLRGCAHYTSCHIYINSPCTPTSNQKPRLHRVSGESIK **(SEQ ID NO: 76)**

atggagtcgctggttttcgcgcggcgctccggccccactccctcggccgcagagctagcccggccgctggcg
gaagggctgatcaagtcgcccaagcccctaatgaagaagcaggcggtgaagcggcaccaccacaagcacaacctgc
ggcaccgctacgagttcctggagaccctgggcaaaggcacctacgggaaggtgaagaaggcgcgggagagctcgg
ggcgcctggtggccatcaagtcaatccggaaggacaaaatcaaagatgagcaagatctgatgcacatacggagggag
attgagatcatgtcatcactcaaccaccctcacatcattgccatccatgaagtgtttgagaacagcagcaagatcgtgatcg
tcatggagtatgccagccggggcgacctttatgactacatcagcgagcggcagcagctcagtgagcgcgaagctaggc
atttcttccggcagatcgtctctgccgtgcactattgccatcagaacagagttgtccaccgagatctcaagctggagaacat
cctcttggatgccaatgggaatatcaagattgctgacttcggtctctccaacctctaccatcaaggcaagttcctgcagaca
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ccctgggtgttctcctctacatcctggtgcatggcaccatgccctttgatgggcatgaccataagatcctagtgaaacagat
cagcaacggggcctaccgggagccacctaaaccctctgcacctgccttttgtcttccagatgcctgtggcctgatccggt
ggctgttgatggtgaaccccacccgccgggccaccctggaggatgtggccagtcactggtgggtcaactggggctacg
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gactggctccggcgttcctcccgccccctcctggagaatggggccaaggtgtgcagcttcttcaagcagcatgcacctg
gtgggggaagcaccacccctggcctggagcgccagcattcgctcaagaagtcccgcaaggagaatgacatggccca
gtctctccacagtgacacggctgatgacactgcccatcgccctggcaagagcaacctcaagctgccaaagggcattctc
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ggcaggctgcccccctgctccccaagaagggcattctcaagaagccccgacagcgcgagtctggctactactcctctcc
cgagcccagtgaatctggggagctcttggacgcaggcgacgtgtttgtgagtggggatcccaaggagcagaagcctcc
gcaagcttcagggctgctcctccatcgcaaaggcatcctcaaactcaatggcaagttctcccagacagccttggagctcg
cggcccccaccaccttcggctccctggatgaactcgccccacctcgccccctggcccgggccagccgaccctcaggg
gctgtgagcgaggacagcatcctgtcctctgagtcctttgaccagctggacttgcctgaacggctcccagagcccccact
gcggggctgtGCTCATTATACCTCCTGCCACATCTATATCAACAGCCCCTGTAC

CCCAACATCTAACCAGAAGCCCCGACTTCACAGGGTCAGTGGAGAATCA
ATAAAA **(SEQ ID NO: 75)**

MOOSE03459 ctg18037 2081197..2081459, 2082567..2082646,
2095897..2095952, 2097096..2097225, 2102594..2102816, 2104449..2104553,
2132126..2132182, 2136635..2136744, 2151478..2151673, 2152506..2152551,
2162130..2162230, 2168807..2168977, 2170668..2170789, 2172867..2173013,
2173674..2173781, 2173923..2174008, 2174759..2174929, 2177037..2177179,
2177933..2177963

MITYTLIKSSLITPQNSGVIFDSPIQARSHVGSTFKIYPKSSISSCLCSYHS
GPSCLHLLSGSFQESSNSYHSLSPCLPTICCQHNSHILSLQASFIVFDSPRNFSD
SPSHSKAKSPMERRAAPRTKLEVYGGLLSSLSSSLVAPVIRSAPATRASLLFP
AVRHVPPAPPEGLRPSRSCSSSVILGRENRCSQAPPSEQQKTSTLRPHFRPPV
GPKGNRCLSHPNSVVRGSPGHFHGKYPSAPTPAVLPKVKQSWQALATGSLS
GRSLLRYIHHAHTSHGERPMLYSNWSQGHPPSSDASQATLLMLRLLLSFCST
TSKSAFCSLTSLHVFLTFHPHFLILSREPGAGPGAGCGAGRAGARAASPSPAP
PKLGGTPTLPTRLAPARPSPERGSKVTTNTATTWSSSTICGTRDIPSEDQEKE
LFLMELFALSRAHLYSQPVSSFNKFSNSSASKQKCVLRETNMASRYEKEFLE
VEKIGVGEFGTVYKCIKRLDGCVYAIKRSMKTFTELSNENSALHEVYAHAV
LGHHPHVVRYYSSWAEDDHMIIQNEYCNGGSLQAAISENTKSGNHFEEPKL
KDILLQISLGLNYIHNSSMVHLDIKPSNIFICHKMQSESSGVIEEVENEADWFL
SANVMYKIGDLGHATSINKPKVEEGDSRFLANEILQEDYRHLPKADIFALGL
TIAVAAGAESLPTNGAAWHHIRKGNFPDVPQELSESFSSLLKNMIQPDAEQR
PSAAALARNTVLRPSLGKTEELQQQLNLEKFKTATLESSVLKAFLSNY **(SEQ ID NO: 78)**

atgatcacttatactttgataaaatcatcacttattacaccccaaaattctggagtcatctttgactcccccattcagg
caagaagtcatgttggctctaccttcaaaatatatccaaaatcaagcatttcttcttgcctctgttcttaccactctggtcccag
ctgccttcatcttttatctggatcattccaggagtcctcaaattcttatcattccctctccccttgcctccctacaatctgttgtca
gcacaacagccacatcctttccttgcaggcttcttttattgtgtttgattctcctagaaatttctctgattctcctagtcattccaa
agcaaagagccccatggagaggagagccgcacccagaaccaagctagaggtttacggaggtctcctctcttccctgtct
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gcaccacctgaaggcctccgccccagtagaagctgcagttcttctgtgatcctaggaagagagaacagatgctcacaag
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gtgcctcagccatcccaacagtgtcgtcagagggtccccagggcattttcatggcaagtacccctctgcccccactccag
cagtgcttcccaaagtgaagcagagctggcaggccttagctacaggctctctctcaggcagatccctttaagatacatac
accatgcccacacatcccatggagagagaccaatgctttattctaactggtcacagggtcacccacctagtagtgatgctt
cccaggctactttgctgatgctgcgtttgcttctgtcattctgctcaaccacttccaaatctgctttttgtagcctcacttctctgc
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gcctggccccggcgcggccctcacccgagcgggggtcgaaggtgaccacgaacacggccaccacctggtcctcctc
caccatttgtgggacgagggatattccctcagaagatcaggaaaaggaactattccttatggaattatttgccctctctaga
gcacatttatactctcaacctgtgtcatctttcaataaattttcaaattcctctgcttccaagcagaaatgtgttttacgagaaac
caacatggcttcccgctatgaaaaagaattcttggaggttgaaaaaattggggttggcgaatttggtacagtctacaagtgc
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catgaagtttatgctcacgcagtgcttgggcatcacccccatgtggtacgttactattcctcatgggcagaagatgaccaca
tgatcattcagaatgaatactgcaatggtgggagtttgcaagctgctatatctgaaaacactaagtctggcaatcattttgaa
gagccaaaactcaaggacatccttctacagatttcccttggccttaattacatccacaactctagcatggtacacctggaca
tcaaacctagtaatatattcatttgtcacaagatgcaaagtgaatcctctggagtcatagaagaagttgaaaatgaagctgat

tggtttctctctgccaatgtgatgtataaaattggtgacctgggccacgcaacatcaataaacaaacccaaagtggaagaa
ggagatagtcgcttcctggctaatgagattttgcaagaggattaccggcaccttcccaaagcagacatatttgccttgggat
taacaattgcagtggctgcaggagcagagtcattgcccaccaatggtgctgcatggcaccatatccgcaagggtaacttt
ccggacgttcctcaggagctctcagaaagcttttccagtctgctcaagaacatgatccaacctgatgccgaacagagacc
ttctgcagcagctctggccagaaatacagttctccggccttccctgggaaaaacagaagagctccaacagcagctgaatt
tggaaaagttcaagactgccacactggaaagcagtgttctgaaggcatttttgagtaattat **(SEQ ID NO: 77)**

MOOSE03283 ctg19153 10113428..10113531, 10144793..10144878,
10150173..10150204, 10157057..10157138, 10159205..10159261,
10162164..10162246, 10164843..10165040, 10179064..10179154,
10187934..10188004, 10189623..10189661, 10194329..10194402,
10195498..10195578, 10196548..10196636

LIDLNGFLMPSILSLKKYFMEHFTLVQRIHETLSQKTKTKQKKKQKKK
KKKKRSSMYEVRSNQTTSHVCYYLCSPYCSITLRTLMHRCLVGVKMVADG
VIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGDA
YTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSD
VDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVAL
NFMKLLIQAGKDSEASILLSSSQCFRIKQDIAEAEELLEPGSFMSPNEIVYPIFQ
EIRRERENSQIPKQASDPPALASQHARITGVSHRTQPTLFLKHSSLNFSD **(SEQ ID NO: 80)**

ctcattgatcttaatggcttccttatgcctagcattctttcgctcaaaaaatatttcatggagcattttacactggtgca
gaggataCACgagactctgtctcaaaaaacaaaaacaaaacaaaaaaaaaaacaaaaaaaaaaaaaaaaaaaaaa
agatcgtcgatgTATgaagttagaagcaaccagaccacctcacatgtctgttactacttatgttccccatattgttctatca
cacttAGGactttgatgcacagatgtttggtgggagtgaaaatgGTTgctgatggagtgatcaaaagcgtattatggc
aaacacttcaagctcttaatttctgtcatatacataactgtattcacagagatataaaacctgaaaatattctaataactaagca
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Aaaattaatcccaagacatcaatcaatctttaaaagtaacgggtttttccatggcatcagtatacctgagccagaagacatg
gaaactcttgaggaaaagttctcagatgttcatcctgtggctctgaacttcatgaagTTATTAATCCAGGCA
GGCAAGGACTCAGAAGCCTCAATTCTACTCAGCTCATCTCAATGCTTCAG
AATTAAGCAGGACATTgctgaggcagaagaattgcttgaacctgggAGTttcatgtcaccaaatgaaat
tgtttatccgatcttccaagaaatcaggagagagagagagaatagccaaatccctaaacaggccAGTgatccacctgc
cttggcctcccaacatgctaggattacaggtgtgagccatcgcacacagccaactcttttcttgaagcattcctctctcaact
tctcagac **(SEQ ID NO:79)**

Table III

ctg14435_MOOSE03013.xml	AGC I Cyclic nucleotide regulated protein kinase family
ctg17872_MOOSE03108.xml	AGC Other AGC-like kinases
ctg15247_MOOSE03109.xml	AGC Other AGC-like kinases
ctg17042_MOOSE03111.xml	AGC Other AGC-like kinases
ctg16439_MOOSE03177.xml	CMGC I Cyclin-dependent kinases (CDKs) and close relatives family
ctg12913_MOOSE03184.xml	CMGC I Cyclin-dependent kinases (CDKs) and close relatives family
ctg17937_MOOSE03219.xml	CMGC II ERK (MAP) kinase family
ctg13541_MOOSE03228.xml	CMGC II ERK (MAP) kinase family
ctg15131_MOOSE03296.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg15131_MOOSE03301.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg16704_MOOSE03304.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg19011_MOOSE03306.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg13286_MOOSE03309.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg13538_MOOSE03312.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg595_MOOSE03313.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg595_MOOSE03314.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg22fin3_MOOSE03316.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg14489_MOOSE03330.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg15907_MOOSE03332.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg16586_MOOSE03340.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg17207_MOOSE03350.xml	CaMK I Kinases regulated by Ca2+/CaM and close relatives family
ctg16775_MOOSE03368.xml	CaMK II KIN1/SNF1/Nim1 family
ctg21fin5_MOOSE03372.xml	CaMK II KIN1/SNF1/Nim1 family
ctg13513_MOOSE03412.xml	OPK IV MEKK/STE11 family
ctg15649_MOOSE03452.xml	OPK V NimA family
ctg15214_MOOSE03453.xml	OPK V NimA family
ctg15214_MOOSE03455.xml	OPK V NimA family

ctg13079_MOOSE03475.xml OPK XI PSK/PTK "mixed lineage" leucine zipper domain family
ctg16734_MOOSE03605.xml PTK XI Eph/Elk/Eck orphan receptor family
ctg16574_MOOSE03608.xml PTK XI Eph/Elk/Eck orphan receptor family
ctg13657_MOOSE03639.xml PTK XVI Insulin receptor family
MOOSE08717 OPK Other - Similar to Other Protein Kinases with no close relatives
MOOSE08757 OPK XII - Casein Kinase I family
MOOSE03397 OPK I - Polo family
MOOSE03609 PTK XI - Eph/Elk/Eck orphan receptor family
MOOSE03184 CMGC I - Cyclin-dependent kinases (CDKs) and close relatives family
MOOSE03305 CaMK I - Kinases regulated by Ca2+/CaM and close relatives family
MOOSE03302 CaMK I - Kinases regulated by Ca2+/CaM and close relatives family
MOOSE03376 CaMK II - KIN1/SNF1/Nim1 family
MOOSE03459 OPK VI - wee1/mik1 family
MOOSE03283 CMGC Other - CMGK kinases

Table IV

KINASES

##########

Parkinson's Disease

Locus1 Marker:D1S231 Lod:5.11 CM_RANGE of one LOD drop:7

MOOSE08888 TK_XI__Eph/Elk/Eck_orphan_receptor_family
DISTANCE: -14.8 Mb

##########

COPD (Chronic Obstructive Pulmonary Disease)

Locus4 Marker:D19S884 Lod:2.9 CM_RANGE of one LOD drop:20

MOOSE08666 OPK_I__Polo_family
DISTANCE: -7.85 Mb

##########

Asthma

Locus2 Marker:D3S1546 Lod:3.4 CM_RANGE of one LOD drop:17

MOOSE08892 PTK_XI__Eph/Elk/Eck_orphan_receptor_family
DISTANCE: -7.75 Mb

##########

NIDDM (Non-insulin dep. Diabetes)

Locus1 Marker:D1S2884 Lod:3.4 CM_RANGE of one LOD drop: 16

MOOSE08580 CaMK_I__Kinases_regulated_by_Ca2+/CaM_and
_close_relatives_family
DISTANCE: 5.785 Mb

MOOSE08888 PTK_XI__Eph/Elk/Eck_orphan_receptor_family
DISTANCE: 12.53 Mb

##########

Migraine (Genomewide scan only)

Locus2 Marker:D2S2321 Lod:2.0 CM_RANGE of one LOD drop:5

MOOSE08409 CMGC_I__Cyclindependent_kinases_(CDKs)_

and_close_relatives_family
DISTANCE: -5.66 Mb

##########

Bipolar (Genomewide scan only)

Locus1	Marker:D1S434	Lod:3.3	CM_RANGE of one LOD drop: 25
	MOOSE08619	CaMK_I__Kinases_regulated_by_Ca2+/CaM_ and_close_relatives_family DISTANCE: -4.43 Mb	

##########

MI (Myocardial Infarction)

Locus4	Marker:D13S1250	Lod:3.2	CM_RANGE of one LOD drop: 5
	MOOSE08757	OPK_XII__Casein_kinase_I_family DISTANCE: 9.668 Mb	

##########

Osteoarthritis

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##########

IBD (Inflammatory Bowel Disease)

Locus3	Marker:D13S1304	Lod:3.2	CM_RANGE of one LOD drop: 15
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CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule comprising a protein kinase gene, wherein the protein kinase gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.

2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.

4. An isolated nucleic molecule which hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, and hybridizes to the first nucleic acid under high stringency conditions.

6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
   (a) the nucleic acid sequences as shown in Tables I and II;
   (b) the complement of one of the nucleic acid sequences are shown in Tables I and II; or

(c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;

where the nucleic acid molecule is operably linked to a regulatory sequence.

7. A recombinant host cell comprising the vector of Claim 6.

8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.

9. An isolated polypeptide encoded by the nucleotide sequence of the group of nucleic acid sequences as shown in Tables I and II, or the complements thereof.

10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

11. An isolated polypeptide comprising an amino acid sequence, wherein the amino acid sequence is greater than about 95% identical to an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.

12. A fusion protein comprising an isolated polypeptide of Claim 2.

13. A fusion protein comprising an isolated polypeptide of Claim 11.

14. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 2, or to a fragment or variant of said amino acid sequence.

15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.

16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

17. A method of identifying an agent which alters the activity of a protein kinase, the method comprising:
    (a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;
    (b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and
    (c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;
    wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a protein kinase.

18. An agent which alters the activity of a protein kinase, identifiable according to the method of Claim 17.

19. The agent of Claim 18, where the agent is selected from the group consisting of: a protein kinase gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

20. A method of altering activity of a polypeptide encoded by a protein kinase gene, comprising contacting the polypeptide with an agent of Claim 19.

21. A method of identifying an agent which alters interaction of the polypeptide of Claim 9 with a protein kinase gene binding agent, comprising:
    a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;
    b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and

c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent that alters interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, identifiable according to the method of Claim 21.

23. An agent which alters interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, selected from the group consisting of: a second protein kinase gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, comprising contacting the protein kinase gene polypeptide and/or the protein kinase gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of a protein kinase gene, comprising the steps of:

a) contacting a solution containing a nucleic acid comprising the promoter region of the protein kinase gene operably linked to a reporter gene with an agent to be tested;

b) assessing the level of expression of the reporter gene; and

c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the protein kinase gene.

26. An agent that alters expression of the protein kinase gene, identifiable according to the method of Claim 25.

27. A method of identifying an agent that alters expression of a protein kinase gene, comprising the steps of:

a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;

b) assessing expression of the nucleic acid, derivative or fragment; and

c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,

wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the protein kinase gene.

28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.

29. An agent that alters expression of a protein kinase gene, identifiable according to the method of Claim 27.

30. An agent that alters expression of a protein kinase gene, selected from the group consisting of: antisense nucleic acid to a protein kinase gene; a protein kinase gene polypeptide; a protein kinase gene receptor; a protein kinase gene binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.

31. A method of altering expression of a protein kinase gene, comprising contacting a cell containing a protein kinase gene with an agent of Claim 30.

32. A method of identifying a polypeptide which interacts with a protein kinase gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a protein kinase gene polypeptide, splicing variant, or a fragment or

derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a protein kinase polypeptide.

33. A protein kinase gene therapeutic agent selected from the group consisting of: a protein kinase gene or fragment or derivative thereof; a polypeptide encoded by a protein kinase gene; a receptor; a protein kinase gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters protein kinase gene expression; an agent that alters activity of a polypeptide encoded by a protein kinase gene; an agent that alters posttranscriptional processing of a polypeptide encoded by a protein kinase gene; an agent that alters interaction of a protein kinase gene with a protein kinase gene binding agent; an agent that alters transcription of splicing variants encoded by a protein kinase gene; and a ribozyme.

34. A pharmaceutical composition comprising a protein kinase gene therapeutic agent of Claim 33.

35. The pharmaceutical composition of Claim 34, wherein the protein kinase gene therapeutic agent is an isolated nucleic acid molecule comprising a protein kinase gene or fragment or derivative thereof.

36. The pharmaceutical composition of Claim 34, wherein the protein kinase gene therapeutic agent is a polypeptide encoded by the protein kinase gene.

37. A method of treating a disease or condition associated with a protein kinase in an individual, comprising administering a protein kinase gene therapeutic agent to the individual, in a therapeutically effective amount.

38. The method of Claim 37, wherein the protein kinase gene therapeutic agent is a protein kinase gene agonist.

39. The method of Claim 38 wherein the protein kinase gene therapeutic agent is a protein kinase gene antagonist.

40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous protein kinase gene and a nucleic acid encoding a protein kinase gene polypeptide.

41. A method for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising:

a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said protein kinase gene nucleic acid under conditions appropriate for hybridization, and

b) assessing whether hybridization has occurred between a protein kinase gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said protein kinase gene nucleic acid;

wherein if hybridization has occurred, a protein kinase gene is present in the nucleic acid.

42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said protein kinase gene nucleic acid.

43. The method of Claim 41, comprising amplification of at least part of said protein kinase gene nucleic acid.

44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said protein kinase gene nucleic acid.

45. A reagent for assaying a sample for the presence of a protein kinase gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous

nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising in separate containers:

a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid, and

b) reagents for detection of said label.

48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid, and which is capable of acting as a primer for said protein kinase gene nucleic acid when maintained under conditions for primer extension.

50. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said protein kinase gene nucleic acid, for assaying a sample for the presence of a protein kinase gene nucleic acid.

51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

c) capable of selectively hybridizing to said protein kinase gene nucleic acid;

for assaying a sample for the presence of a protein kinase gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;

b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or

c) capable of selectively hybridizing to said protein kinase gene nucleic acid;

for diagnosing a susceptibility to a disease or condition associated with a protein kinase.

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Sigurdsson, Gunnar Thor

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aag gcc gag agg gac atc ctg gcc gag gca gac aat gag tgg gtg gtc   528
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gac tac atc cct ggt ggg gac atg atg agc ctg ctg atc cgg atg gag   624
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ttc ggc ctc tgc act ggg ttc agg tgc ctg gca cat tca ctg gtg ggg   816
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caa ctc tgt gac tgg tgg agt gtt gga gtg att ctc ttc gag atg ctg   912
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    50                  55                  60

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Ile Lys Arg Glu Arg Pro Ala Arg Glu Leu Pro Gly Gln Arg Gly Ile
65                  70                  75                  80

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Leu Ser Leu Ile Ile Thr Ala Asp Asp Gly Ser Gly Gly Pro Leu Met
465                 470                 475                 480

agc ccc ctt tcc ccg cgc tct ctg tcc tcg aac ccg tcg tcc cgt gac   1488
Ser Pro Leu Ser Pro Arg Ser Leu Ser Ser Asn Pro Ser Ser Arg Asp
                485                 490                 495

tct tcg ccg agc cga gac ccg tcc ccc gtg tgt ggc agc ctg cgg ccc   1536
Ser Ser Pro Ser Arg Asp Pro Ser Pro Val Cys Gly Ser Leu Arg Pro
            500                 505                 510

ccc atc gtt atc cac agc tct ggc aag aag tac ggc ttc agc ctg cgg   1584
Pro Ile Val Ile His Ser Ser Gly Lys Lys Tyr Gly Phe Ser Leu Arg
        515                 520                 525

gcg atc cgc gtc tac atg ggt gat agc gac gtc tac act gtg cac cac   1632
Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr Val His His
    530                 535                 540

gtc gtc tgg agt gtg gag gac gga agc ccc gcc cag gag gcg ggc ctg   1680
Val Val Trp Ser Val Glu Asp Gly Ser Pro Ala Gln Glu Ala Gly Leu
545                 550                 555                 560

cgg gct ggg gac ctc atc acc cac atc aac ggg gag tca gtg ctg ggg   1728
Arg Ala Gly Asp Leu Ile Thr His Ile Asn Gly Glu Ser Val Leu Gly
                565                 570                 575

ctg gtg cac atg gac gtc gtg gag ctg ctg ctg aag agc ggc aac aag   1776
Leu Val His Met Asp Val Val Glu Leu Leu Leu Lys Ser Gly Asn Lys
            580                 585                 590

ata tcc ctg cgg acc aca gcc ctg gag aac acc tcc atc aag gtg ggc   1824
Ile Ser Leu Arg Thr Thr Ala Leu Glu Asn Thr Ser Ile Lys Val Gly
        595                 600                 605

ccc gcc cgg aag aat gtg gcc aag ggc cgc atg gca cgc agg agc aag   1872
Pro Ala Arg Lys Asn Val Ala Lys Gly Arg Met Ala Arg Arg Ser Lys
    610                 615                 620
```

```
agg agc cgt cgg cgg gag acc cag gat cgg cgg aag tca ctt ttc aag   1920
Arg Ser Arg Arg Arg Glu Thr Gln Asp Arg Arg Lys Ser Leu Phe Lys
625                 630                 635                 640

aag atc tcc aag cag acc tcc gtg ctg cac acc agc cgc agc ttc tcc   1968
Lys Ile Ser Lys Gln Thr Ser Val Leu His Thr Ser Arg Ser Phe Ser
                645                 650                 655

tcc gga ctc cac cac tca ctg tca tcc agt gag agc ctc ccc ggc tcg   2016
Ser Gly Leu His His Ser Leu Ser Ser Ser Glu Ser Leu Pro Gly Ser
            660                 665                 670

ccc acc cac agc ctc tcc ccc agc ccc acc act ccc tgc cga agc cca   2064
Pro Thr His Ser Leu Ser Pro Ser Pro Thr Thr Pro Cys Arg Ser Pro
        675                 680                 685

gcc cct gat gtc cca gca gat acc act gca tcc cca ccc agc gca tcc   2112
Ala Pro Asp Val Pro Ala Asp Thr Thr Ala Ser Pro Pro Ser Ala Ser
    690                 695                 700

ccg agc tcc agc agc ccc gcc tcc cca gct gct gct ggc cac acc cgc   2160
Pro Ser Ser Ser Ser Pro Ala Ser Pro Ala Ala Ala Gly His Thr Arg
705                 710                 715                 720

ccc agc tcc ctg cac ggc ctg gct gcc aag ctt ggg cca ccc cgc ccc   2208
Pro Ser Ser Leu His Gly Leu Ala Ala Lys Leu Gly Pro Pro Arg Pro
                725                 730                 735

aag act ggc cgc cgc aag tcc acc agc agc atc ccg ccc tcc ccg ctg   2256
Lys Thr Gly Arg Arg Lys Ser Thr Ser Ser Ile Pro Pro Ser Pro Leu
            740                 745                 750

gcc tgc ccg ccc atc tcc gcg ccc cca ccc cgc tcg ccc tcg ccc ctg   2304
Ala Cys Pro Pro Ile Ser Ala Pro Pro Pro Arg Ser Pro Ser Pro Leu
        755                 760                 765

ccc ggg cac ccg ccc gca cct gcc cga tcc ccg cgg ctg cgc cgg ggc   2352
Pro Gly His Pro Pro Ala Pro Ala Arg Ser Pro Arg Leu Arg Arg Gly
    770                 775                 780

cag tca gct gac aag ctg ggc aca ggg gag cgg ctg gat ggg gag gcg   2400
Gln Ser Ala Asp Lys Leu Gly Thr Gly Glu Arg Leu Asp Gly Glu Ala
785                 790                 795                 800

ggg cgg cgc act cgt ggg cca gag gcc gag ctc gtg gtc atg cgg cgg   2448
Gly Arg Arg Thr Arg Gly Pro Glu Ala Glu Leu Val Val Met Arg Arg
                805                 810                 815

ctg cac ctg tcc gag cgc cga gac tcc ttc aag aag cag gag gcc gtg   2496
Leu His Leu Ser Glu Arg Arg Asp Ser Phe Lys Lys Gln Glu Ala Val
            820                 825                 830

cag gag gtt agc ttc gat gag ccg cag gag gag gcc act ggg ctg ccc   2544
Gln Glu Val Ser Phe Asp Glu Pro Gln Glu Glu Ala Thr Gly Leu Pro
        835                 840                 845

acc tca gtg cca cag atc gcc gtg gag ggc gag gaa gcc act gag gca   2592
Thr Ser Val Pro Gln Ile Ala Val Glu Gly Glu Glu Ala Thr Glu Ala
    850                 855                 860
```

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cag aac cga cag ctg ccc tcc acc acg cgt ggc ctc atg gcg tct ttg   2640
Gln Asn Arg Gln Leu Pro Ser Thr Thr Arg Gly Leu Met Ala Ser Leu
865                 870                 875                 880

act tgg act cct gtt tac cac cct ccc cat cac acc cag aat cca cac   2688
Thr Trp Thr Pro Val Tyr His Pro Pro His His Thr Gln Asn Pro His
                885                 890                 895

ccc cac tgc gac gtc att gtc cct tca gcc ctc ccc aac cct ggg gcc   2736
Pro His Cys Asp Val Ile Val Pro Ser Ala Leu Pro Asn Pro Gly Ala
            900                 905                 910

tca ctg tcc ttg tct tgc ctg cag ctc tac gcc cca ggg ctg tcg cca   2784
Ser Leu Ser Leu Ser Cys Leu Gln Leu Tyr Ala Pro Gly Leu Ser Pro
        915                 920                 925

gac act atc atg gag tgt gca atg ggg gac cgc ggc atg cag ctc atg   2832
Asp Thr Ile Met Glu Cys Ala Met Gly Asp Arg Gly Met Gln Leu Met
    930                 935                 940

cac gcc aac gcc cag cgg aca gat gct ctc cag cca cca cac gaa gag   2880
His Ala Asn Ala Gln Arg Thr Asp Ala Leu Gln Pro Pro His Glu Glu
945                 950                 955                 960

tct cct gcc tca gcc tcc cga gta gct ggg act aca agc ggg tgc tac   2928
Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Thr Thr Ser Gly Cys Tyr
                965                 970                 975

cac acc tgg cta ttt ttt ttt ttt tat gag ccg aga tcg cgc cac tgc   2976
His Thr Trp Leu Phe Phe Phe Phe Tyr Glu Pro Arg Ser Arg His Cys
            980                 985                 990

act cca gcc tgg gcg aca gtt cga gac tcc gtc tca aac aaa caa aaa   3024
Thr Pro Ala Trp Ala Thr Val Arg Asp Ser Val Ser Asn Lys Gln Lys
        995                 1000                1005

gac cca acc ctt ctc tgc tca ttc ggt cca agt atg acc ggg tct gag   3072
Asp Pro Thr Leu Leu Cys Ser Phe Gly Pro Ser Met Thr Gly Ser Glu
    1010                1015                1020

ttg ggt ctg atc acg tcg aat tgg act tgg tca cga aga gtt tgt tcg   3120
Leu Gly Leu Ile Thr Ser Asn Trp Thr Trp Ser Arg Arg Val Cys Ser
1025                1030                1035                1040

atg acc tca gcc cgt ccc act ctg ggc ctc aca                      3153
Met Thr Ser Ala Arg Pro Thr Leu Gly Leu Thr
                1045                1050
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<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

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Leu Glu Gly Glu Val Glu Thr Arg His Ser Glu Val Thr Ala Ser Cys
 1               5                  10                  15
Val Leu Cys Pro Arg Ala Arg Pro Leu Pro Ala Pro Gly Val Gly Arg
            20                  25                  30
Ser Arg Gly Leu Gly Ala Asp Gln Gly Asn Arg Cys Pro Pro Ser Gly
        35                  40                  45
```

```
Ser Ser Thr His Ile Ser Leu Leu Glu Ala Glu Val Pro Gly Val Thr
    50                  55                  60
Ile Lys Arg Glu Arg Pro Ala Arg Glu Leu Pro Gly Gln Arg Gly Ile
65                  70                  75                  80
Arg Glu Gly Ala Tyr Met Ala Val Tyr Leu Val Arg His Arg Asp Thr
                85                  90                  95
Arg Gln Arg Phe Ala Ile Lys Lys Ile Asn Lys Gln Asn Leu Ile Leu
            100                 105                 110
Arg Asn Gln Ile Gln Gln Val Phe Val Glu Arg Asp Ile Leu Thr Phe
        115                 120                 125
Ala Glu Asn Pro Phe Val Val Ser Met Phe Cys Ser Phe Glu Thr Arg
    130                 135                 140
Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly Gly Asp Cys Ala
145                 150                 155                 160
Thr Leu Leu Lys Asn Met Gly Pro Leu Pro Val Asp Met Ala Arg Leu
                165                 170                 175
Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu His Asn Tyr Gly
            180                 185                 190
Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu Ile Thr Ser Leu
        195                 200                 205
Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Ile Gly Leu Met
    210                 215                 220
Ser Met Ala Thr Asn Leu Tyr Glu Gly His Ile Glu Lys Asp Ala Arg
225                 230                 235                 240
Glu Phe Ile Asp Lys Gln Val Cys Gly Thr Pro Glu Tyr Ile Ala Pro
                245                 250                 255
Glu Val Ile Phe Arg Gln Gly Tyr Gly Lys Pro Val Asp Trp Trp Ala
            260                 265                 270
Met Gly Val Val Leu Tyr Glu Phe Leu Val Gly Cys Val Pro Phe Phe
        275                 280                 285
Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln Val Val Ser Asp Glu Ile
    290                 295                 300
Met Trp Pro Glu Gly Asp Glu Ala Leu Pro Ala Asp Ala Gln Asp Leu
305                 310                 315                 320
Ile Thr Arg Leu Leu Arg Gln Ser Pro Leu Asp Arg Leu Gly Thr Gly
                325                 330                 335
Gly Thr His Glu Val Lys Gln His Pro Phe Phe Leu Ala Leu Asp Trp
            340                 345                 350
Ala Gly Leu Leu Arg His Lys Ala Glu Phe Val Pro Gln Leu Glu Ala
        355                 360                 365
Glu Asp Asp Thr Ser Tyr Phe Asp Thr Arg Ser Glu Arg Tyr Arg His
    370                 375                 380
Leu Gly Ser Glu Asp Asp Glu Thr Asn Asp Glu Glu Ser Ser Thr Glu
385                 390                 395                 400
Ile Pro Gln Phe Ser Ser Cys Ser His Arg Phe Ser Lys Val Tyr Ser
                405                 410                 415
Ser Ser Glu Phe Leu Ala Val Gln Pro Thr Pro Thr Phe Ala Glu Arg
            420                 425                 430
Ser Phe Ser Glu Asp Arg Glu Glu Gly Ala Ser Ser Ser Gly Gly Ser
        435                 440                 445
Gly Gly Gly Ser Gly Gly Arg Val Pro Lys Ser Ala Ser Val Ser Ala
    450                 455                 460
Leu Ser Leu Ile Ile Thr Ala Asp Asp Gly Ser Gly Gly Pro Leu Met
465                 470                 475                 480
Ser Pro Leu Ser Pro Arg Ser Leu Ser Ser Asn Pro Ser Ser Arg Asp
                485                 490                 495
Ser Ser Pro Ser Arg Asp Pro Ser Pro Val Cys Gly Ser Leu Arg Pro
            500                 505                 510
Pro Ile Val Ile His Ser Ser Gly Lys Lys Tyr Gly Phe Ser Leu Arg
        515                 520                 525
Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr Val His His
    530                 535                 540
```

```
Val Val Trp Ser Val Glu Asp Gly Ser Pro Ala Gln Glu Ala Gly Leu
545                 550                 555                 560
Arg Ala Gly Asp Leu Ile Thr His Ile Asn Gly Glu Ser Val Leu Gly
                565                 570                 575
Leu Val His Met Asp Val Val Glu Leu Leu Leu Lys Ser Gly Asn Lys
            580                 585                 590
Ile Ser Leu Arg Thr Thr Ala Leu Glu Asn Thr Ser Ile Lys Val Gly
        595                 600                 605
Pro Ala Arg Lys Asn Val Ala Lys Gly Arg Met Ala Arg Arg Ser Lys
    610                 615                 620
Arg Ser Arg Arg Arg Glu Thr Gln Asp Arg Arg Lys Ser Leu Phe Lys
625                 630                 635                 640
Lys Ile Ser Lys Gln Thr Ser Val Leu His Thr Ser Arg Ser Phe Ser
                645                 650                 655
Ser Gly Leu His His Ser Leu Ser Ser Ser Glu Ser Leu Pro Gly Ser
            660                 665                 670
Pro Thr His Ser Leu Ser Pro Ser Pro Thr Thr Pro Cys Arg Ser Pro
        675                 680                 685
Ala Pro Asp Val Pro Ala Asp Thr Thr Ala Ser Pro Pro Ser Ala Ser
    690                 695                 700
Pro Ser Ser Ser Ser Pro Ala Ser Pro Ala Ala Ala Gly His Thr Arg
705                 710                 715                 720
Pro Ser Ser Leu His Gly Leu Ala Ala Lys Leu Gly Pro Pro Arg Pro
                725                 730                 735
Lys Thr Gly Arg Arg Lys Ser Thr Ser Ser Ile Pro Pro Ser Pro Leu
            740                 745                 750
Ala Cys Pro Pro Ile Ser Ala Pro Pro Pro Arg Ser Pro Ser Pro Leu
        755                 760                 765
Pro Gly His Pro Pro Ala Pro Ala Arg Ser Pro Arg Leu Arg Arg Gly
    770                 775                 780
Gln Ser Ala Asp Lys Leu Gly Thr Gly Glu Arg Leu Asp Gly Glu Ala
785                 790                 795                 800
Gly Arg Arg Thr Arg Gly Pro Glu Ala Glu Leu Val Val Met Arg Arg
                805                 810                 815
Leu His Leu Ser Glu Arg Arg Asp Ser Phe Lys Lys Gln Glu Ala Val
            820                 825                 830
Gln Glu Val Ser Phe Asp Glu Pro Gln Glu Glu Ala Thr Gly Leu Pro
        835                 840                 845
Thr Ser Val Pro Gln Ile Ala Val Glu Gly Glu Glu Ala Thr Glu Ala
    850                 855                 860
Gln Asn Arg Gln Leu Pro Ser Thr Thr Arg Gly Leu Met Ala Ser Leu
865                 870                 875                 880
Thr Trp Thr Pro Val Tyr His Pro Pro His His Thr Gln Asn Pro His
                885                 890                 895
Pro His Cys Asp Val Ile Val Pro Ser Ala Leu Pro Asn Pro Gly Ala
            900                 905                 910
Ser Leu Ser Leu Ser Cys Leu Gln Leu Tyr Ala Pro Gly Leu Ser Pro
        915                 920                 925
Asp Thr Ile Met Glu Cys Ala Met Gly Asp Arg Gly Met Gln Leu Met
    930                 935                 940
His Ala Asn Ala Gln Arg Thr Asp Ala Leu Gln Pro Pro His Glu Glu
945                 950                 955                 960
Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Thr Thr Ser Gly Cys Tyr
                965                 970                 975
His Thr Trp Leu Phe Phe Phe Phe Tyr Glu Pro Arg Ser Arg His Cys
            980                 985                 990
Thr Pro Ala Trp Ala Thr Val Arg Asp Ser Val Ser Asn Lys Gln Lys
        995                 1000                1005
Asp Pro Thr Leu Leu Cys Ser Phe Gly Pro Ser Met Thr Gly Ser Glu
    1010                1015                1020
Leu Gly Leu Ile Thr Ser Asn Trp Thr Trp Ser Arg Arg Val Cys Ser
1025                1030                1035                1040
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Met Thr Ser Ala Arg Pro Thr Leu Gly Leu Thr
                1045                1050


<210> 5
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<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(2157)
<223> MOOSE03109

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att tct gtt gaa tgt cat aaa agg aga ttt ggt ggt cac gga agt aaa   48
Ile Ser Val Glu Cys His Lys Arg Arg Phe Gly Gly His Gly Ser Lys
 1               5                  10                  15

ccc cct tcc ctt ttg tgg gtc aaa aag aag tgg tcc ttg ggt cct cgg   96
Pro Pro Ser Leu Leu Trp Val Lys Lys Lys Trp Ser Leu Gly Pro Arg
            20                  25                  30

aag cag aag gaa gga aga gac cct ttt att ttt ttg gtt agt gaa tgt   144
Lys Gln Lys Glu Gly Arg Asp Pro Phe Ile Phe Leu Val Ser Glu Cys
        35                  40                  45

cag cca cca atg aca cgt gct aat act atg aca tca gag ccc acc atg   192
Gln Pro Pro Met Thr Arg Ala Asn Thr Met Thr Ser Glu Pro Thr Met
    50                  55                  60

tta gcc att tgc cga aca agc aac cgg aaa agc tta ata ggc aat ggg   240
Leu Ala Ile Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Gly Asn Gly
65                  70                  75                  80

cag tca cca gca ttg cct cga cca cac tca cct ctc tct gct cat gca   288
Gln Ser Pro Ala Leu Pro Arg Pro His Ser Pro Leu Ser Ala His Ala
                85                  90                  95

ggt aat tgc cct caa gat agt cca aga aat ttc tcc ccc agt gcc tca   336
Gly Asn Cys Pro Gln Asp Ser Pro Arg Asn Phe Ser Pro Ser Ala Ser
            100                 105                 110

gcc cat ttt tca ttt gca cgg agg act gat gga cgc cgc tgg tcg ttg   384
Ala His Phe Ser Phe Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu
        115                 120                 125

gct tct ctc cct tcc tct ggc tat ggg aca aac aca ccc agc tct acg   432
Ala Ser Leu Pro Ser Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr
    130                 135                 140

gtc tct tca tcc tgt tcc tcc cag gag aag ttg cat cag tta cca tac   480
Val Ser Ser Ser Cys Ser Ser Gln Glu Lys Leu His Gln Leu Pro Tyr
145                 150                 155                 160

caa cca aca cca gac gag tta cac ttc tta tca aaa cat ttc tgt acc   528
Gln Pro Thr Pro Asp Glu Leu His Phe Leu Ser Lys His Phe Cys Thr
                165                 170                 175

acc gaa agc atc gcc act gag aac aga tgc agg aac acg ccg atg cgc   576
Thr Glu Ser Ile Ala Thr Glu Asn Arg Cys Arg Asn Thr Pro Met Arg
            180                 185                 190
```

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ccc cgt tcc cga agt ctg agc cct gga cgt tct ccc gcc tgc tgt gac   624
Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg Ser Pro Ala Cys Cys Asp
        195                 200                 205

cat gaa ata att atg atg aac cat gtc tac aaa gaa agg ttc cca aag   672
His Glu Ile Ile Met Met Asn His Val Tyr Lys Glu Arg Phe Pro Lys
    210                 215                 220

gct aca gct cag atg gaa gaa cgt cta aag gaa att atc acc agc tac   720
Ala Thr Ala Gln Met Glu Glu Arg Leu Lys Glu Ile Ile Thr Ser Tyr
225                 230                 235                 240

tct cct gac aac gtt cta ccc tta gca gat gga gtg ctt agt ttc act   768
Ser Pro Asp Asn Val Leu Pro Leu Ala Asp Gly Val Leu Ser Phe Thr
                245                 250                 255

cac cac cag att att gaa ctg gct cga gat tgc ttg gat aaa tcc cac   816
His His Gln Ile Ile Glu Leu Ala Arg Asp Cys Leu Asp Lys Ser His
            260                 265                 270

cag ggc ctc atc acc tca cga tac ttc ctt gaa tta cag cac aaa tta   864
Gln Gly Leu Ile Thr Ser Arg Tyr Phe Leu Glu Leu Gln His Lys Leu
        275                 280                 285

gat aag ttg cta cag gag gct cat gat cgt tca gaa agt gga gaa ttg   912
Asp Lys Leu Leu Gln Glu Ala His Asp Arg Ser Glu Ser Gly Glu Leu
    290                 295                 300

gca ttt att aaa caa cta gtt cga aag atc cta att gtt att gcc cgc   960
Ala Phe Ile Lys Gln Leu Val Arg Lys Ile Leu Ile Val Ile Ala Arg
305                 310                 315                 320

cct gct cgg tta tta gag tgc ctg gaa ttt gat ccg gaa gaa ttt tac  1008
Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr
                325                 330                 335

tac cta ttg gaa gca gca gaa ggc cat gcc aaa gaa gga cag ggt att  1056
Tyr Leu Leu Glu Ala Ala Glu Gly His Ala Lys Glu Gly Gln Gly Ile
            340                 345                 350

aaa acc gac att ccc agg tac atc att agc caa ctg gga ctc aat aag  1104
Lys Thr Asp Ile Pro Arg Tyr Ile Ile Ser Gln Leu Gly Leu Asn Lys
        355                 360                 365

gat ccc ttg gaa gaa atg gct cat ttg gga aac tac gat agt ggg aca  1152
Asp Pro Leu Glu Glu Met Ala His Leu Gly Asn Tyr Asp Ser Gly Thr
    370                 375                 380

gca gaa aca cca gaa aca gat gaa tca gtg agt agc tct aat gcc tcc  1200
Ala Glu Thr Pro Glu Thr Asp Glu Ser Val Ser Ser Ser Asn Ala Ser
385                 390                 395                 400

ctg aaa ctt cga agg aaa cct cgg gaa agt gat ttt gaa acg att aaa  1248
Leu Lys Leu Arg Arg Lys Pro Arg Glu Ser Asp Phe Glu Thr Ile Lys
                405                 410                 415

ttg att agc aat gga gcc tat ggg gca gtc tac ttt gtt cgg cat aaa  1296
Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Tyr Phe Val Arg His Lys
            420                 425                 430
```

```
gaa tcc cgg cag agg ttt gcc atg aag aag att aat aaa cag aac ctc   1344
Glu Ser Arg Gln Arg Phe Ala Met Lys Lys Ile Asn Lys Gln Asn Leu
        435                 440                 445

atc ctt cga aac cag atc cag cag gcc ttt gtg gag cgg gat atc ctg   1392
Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu Arg Asp Ile Leu
    450                 455                 460

act ttt gca gaa aac ccc ttt gtt gtc agc atg tat tgc tcc ttt gaa   1440
Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Tyr Cys Ser Phe Glu
465                 470                 475                 480

aca agg cgc cac ttg tgc atg gtc atg gaa tat gtg gaa ggg gga gac   1488
Thr Arg Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly Gly Asp
                485                 490                 495

tgt gct act tta atg aaa aac atg ggt cct ctc cct gtt gat atg gcc   1536
Cys Ala Thr Leu Met Lys Asn Met Gly Pro Leu Pro Val Asp Met Ala
            500                 505                 510

aga atg tac ttt gct gag acg gtc ttg gcc ttg gaa tat tta cat aat   1584
Arg Met Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu His Asn
        515                 520                 525

tat gga att gta cac agg gat ttg aaa cca gac aac ttg ttg gtt acc   1632
Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu Val Thr
    530                 535                 540

tcc atg ggg cac ata aag ctg aca gat ttt gga tta tct aag gtg gga   1680
Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Val Gly
545                 550                 555                 560

cta atg agc atg act acc aac ctt tac gag ggt cat att gag aag gat   1728
Leu Met Ser Met Thr Thr Asn Leu Tyr Glu Gly His Ile Glu Lys Asp
                565                 570                 575

gct aga gag ttc ctg gat aaa cag gtc tgt ggc aca cct gaa tac att   1776
Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr Pro Glu Tyr Ile
            580                 585                 590

gca cca gaa gtg att ctg agg cag ggt tat gga aag ccg gtg gac tgg   1824
Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys Pro Val Asp Trp
        595                 600                 605

tgg gcc atg ggg att atc ctc tat gaa ttt ctg gtt gga tgc gtg cca   1872
Trp Ala Met Gly Ile Ile Leu Tyr Glu Phe Leu Val Gly Cys Val Pro
    610                 615                 620

ttc ttt ggg gat act cca gag gag cta ttt gga caa gtc atc agt gat   1920
Phe Phe Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln Val Ile Ser Asp
625                 630                 635                 640

gag atc aac tgg cct gag aag gat gag gca ccc cca cct gat gcc cag   1968
Glu Ile Asn Trp Pro Glu Lys Asp Glu Ala Pro Pro Pro Asp Ala Gln
                645                 650                 655

gat ctg att acc tta ctc ctc agg cag aat ccc ctg gag agg ctg gga   2016
Asp Leu Ile Thr Leu Leu Leu Arg Gln Asn Pro Leu Glu Arg Leu Gly
            660                 665                 670
```

```
aca ggt ggt gca tat gaa gtc aaa cag cat cga ttc ttc cgt tct tta   2064
Thr Gly Gly Ala Tyr Glu Val Lys Gln His Arg Phe Phe Arg Ser Leu
        675                 680                 685

gac tgg aac agt ttg ctg aga cag aag gca gaa ttt att ccc caa ctg   2112
Asp Trp Asn Ser Leu Leu Arg Gln Lys Ala Glu Phe Ile Pro Gln Leu
    690                 695                 700

gaa tct gag gat gac aca agt tat ttt gat agt atg tgc ttt atc       2157
Glu Ser Glu Asp Asp Thr Ser Tyr Phe Asp Ser Met Cys Phe Ile
705                 710                 715
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<210> 6
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<212> PRT
<213> Homo sapiens

<400> 6

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Ile Ser Val Glu Cys His Lys Arg Arg Phe Gly Gly His Gly Ser Lys
 1               5                  10                  15
Pro Pro Ser Leu Leu Trp Val Lys Lys Lys Trp Ser Leu Gly Pro Arg
            20                  25                  30
Lys Gln Lys Glu Gly Arg Asp Pro Phe Ile Phe Leu Val Ser Glu Cys
        35                  40                  45
Gln Pro Pro Met Thr Arg Ala Asn Thr Met Thr Ser Glu Pro Thr Met
    50                  55                  60
Leu Ala Ile Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Gly Asn Gly
65                  70                  75                  80
Gln Ser Pro Ala Leu Pro Arg Pro His Ser Pro Leu Ser Ala His Ala
                85                  90                  95
Gly Asn Cys Pro Gln Asp Ser Pro Arg Asn Phe Ser Pro Ser Ala Ser
            100                 105                 110
Ala His Phe Ser Phe Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu
        115                 120                 125
Ala Ser Leu Pro Ser Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr
    130                 135                 140
Val Ser Ser Ser Cys Ser Ser Gln Glu Lys Leu His Gln Leu Pro Tyr
145                 150                 155                 160
Gln Pro Thr Pro Asp Glu Leu His Phe Leu Ser Lys His Phe Cys Thr
                165                 170                 175
Thr Glu Ser Ile Ala Thr Glu Asn Arg Cys Arg Asn Thr Pro Met Arg
            180                 185                 190
Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg Ser Pro Ala Cys Cys Asp
        195                 200                 205
His Glu Ile Ile Met Met Asn His Val Tyr Lys Glu Arg Phe Pro Lys
    210                 215                 220
Ala Thr Ala Gln Met Glu Glu Arg Leu Lys Glu Ile Ile Thr Ser Tyr
225                 230                 235                 240
Ser Pro Asp Asn Val Leu Pro Leu Ala Asp Gly Val Leu Ser Phe Thr
                245                 250                 255
His His Gln Ile Ile Glu Leu Ala Arg Asp Cys Leu Asp Lys Ser His
            260                 265                 270
Gln Gly Leu Ile Thr Ser Arg Tyr Phe Leu Glu Leu Gln His Lys Leu
        275                 280                 285
Asp Lys Leu Leu Gln Glu Ala His Asp Arg Ser Glu Ser Gly Glu Leu
    290                 295                 300
Ala Phe Ile Lys Gln Leu Val Arg Lys Ile Leu Ile Val Ile Ala Arg
305                 310                 315                 320
Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr
                325                 330                 335
```

```
Tyr Leu Leu Glu Ala Ala Glu Gly His Ala Lys Glu Gly Gln Gly Ile
            340                 345                 350
Lys Thr Asp Ile Pro Arg Tyr Ile Ile Ser Gln Leu Gly Leu Asn Lys
        355                 360                 365
Asp Pro Leu Glu Glu Met Ala His Leu Gly Asn Tyr Asp Ser Gly Thr
    370                 375                 380
Ala Glu Thr Pro Glu Thr Asp Glu Ser Val Ser Ser Ser Asn Ala Ser
385                 390                 395                 400
Leu Lys Leu Arg Arg Lys Pro Arg Glu Ser Asp Phe Glu Thr Ile Lys
                405                 410                 415
Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Tyr Phe Val Arg His Lys
            420                 425                 430
Glu Ser Arg Gln Arg Phe Ala Met Lys Lys Ile Asn Lys Gln Asn Leu
        435                 440                 445
Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu Arg Asp Ile Leu
    450                 455                 460
Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Tyr Cys Ser Phe Glu
465                 470                 475                 480
Thr Arg Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly Gly Asp
                485                 490                 495
Cys Ala Thr Leu Met Lys Asn Met Gly Pro Leu Pro Val Asp Met Ala
            500                 505                 510
Arg Met Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu His Asn
        515                 520                 525
Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu Val Thr
    530                 535                 540
Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Val Gly
545                 550                 555                 560
Leu Met Ser Met Thr Thr Asn Leu Tyr Glu Gly His Ile Glu Lys Asp
                565                 570                 575
Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr Pro Glu Tyr Ile
            580                 585                 590
Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys Pro Val Asp Trp
        595                 600                 605
Trp Ala Met Gly Ile Ile Leu Tyr Glu Phe Leu Val Gly Cys Val Pro
    610                 615                 620
Phe Phe Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln Val Ile Ser Asp
625                 630                 635                 640
Glu Ile Asn Trp Pro Glu Lys Asp Glu Ala Pro Pro Pro Asp Ala Gln
                645                 650                 655
Asp Leu Ile Thr Leu Leu Leu Arg Gln Asn Pro Leu Glu Arg Leu Gly
            660                 665                 670
Thr Gly Gly Ala Tyr Glu Val Lys Gln His Arg Phe Phe Arg Ser Leu
        675                 680                 685
Asp Trp Asn Ser Leu Leu Arg Gln Lys Ala Glu Phe Ile Pro Gln Leu
    690                 695                 700
Glu Ser Glu Asp Asp Thr Ser Tyr Phe Asp Ser Met Cys Phe Ile
705                 710                 715
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<210> 7
<211> 2463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2463)
<223> MOOSE03111

<400> 7

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atg gag cgg cgg ctg cgc gcg ctg gag cag ctg gcg cgg ggc gag gcc   48
Met Glu Arg Arg Leu Arg Ala Leu Glu Gln Leu Ala Arg Gly Glu Ala
 1               5                  10                  15

ggc ggc tgc ccg ggg ctc gac ggc ctc cta gat ctg ctg ctg gcg ctg   96
Gly Gly Cys Pro Gly Leu Asp Gly Leu Leu Asp Leu Leu Leu Ala Leu
            20                  25                  30

cac cac gag ctc agc agc ggc ccc cta cgg cgg gag cgc agc gtg gcg   144
His His Glu Leu Ser Ser Gly Pro Leu Arg Arg Glu Arg Ser Val Ala
        35                  40                  45

cag ttc ctg agc tgg gcc agc ccc ttc gta tca aag gtg aaa gaa ctg   192
Gln Phe Leu Ser Trp Ala Ser Pro Phe Val Ser Lys Val Lys Glu Leu
    50                  55                  60

cgt ctg cag aga gat gac ttt gag atc ttg aag gtg atc ggc cga gga   240
Arg Leu Gln Arg Asp Asp Phe Glu Ile Leu Lys Val Ile Gly Arg Gly
65                  70                  75                  80

gcc ttt ggg gag gtc acc gtg gtg agg cag agg gac act ggg cag att   288
Ala Phe Gly Glu Val Thr Val Val Arg Gln Arg Asp Thr Gly Gln Ile
                85                  90                  95

ttt gcc atg aaa atg ctg cac aag tgg gag atg ctg aag agg gct gag   336
Phe Ala Met Lys Met Leu His Lys Trp Glu Met Leu Lys Arg Ala Glu
            100                 105                 110

gtc acc tgt ttc cgg gag gag cgg gat gtg ctc gtg aaa ggg gac agc   384
Val Thr Cys Phe Arg Glu Glu Arg Asp Val Leu Val Lys Gly Asp Ser
        115                 120                 125

cgt tgg gtg acc act ctg cac tat gcc ttc caa gac gag gag tac ctg   432
Arg Trp Val Thr Thr Leu His Tyr Ala Phe Gln Asp Glu Glu Tyr Leu
    130                 135                 140

tac ctt gtg atg gac tac tat gct ggt ggg gac ctc ctg acg ctg ctg   480
Tyr Leu Val Met Asp Tyr Tyr Ala Gly Gly Asp Leu Leu Thr Leu Leu
145                 150                 155                 160

agc cgc ttc gag gac cgt ctc ccg ccc gag ctg gcc cag ttc tac ctg   528
Ser Arg Phe Glu Asp Arg Leu Pro Pro Glu Leu Ala Gln Phe Tyr Leu
                165                 170                 175

gct gag atg gtg ctg gcc atc cac tcg ctg cac cag ctg ggt tat gtc   576
Ala Glu Met Val Leu Ala Ile His Ser Leu His Gln Leu Gly Tyr Val
            180                 185                 190

cac agg gat gtc aag cca gac aac gtc ctg ctg gat gtg aac ggg cac   624
His Arg Asp Val Lys Pro Asp Asn Val Leu Leu Asp Val Asn Gly His
        195                 200                 205

att cgc ctg gct gac ttc ggc tcc tgc ctg cgt ctc aac acc aac ggc   672
Ile Arg Leu Ala Asp Phe Gly Ser Cys Leu Arg Leu Asn Thr Asn Gly
    210                 215                 220

atg gtg gat tca tca gtg gca gta ggg acg ccg gac tat atc tcc cct   720
Met Val Asp Ser Ser Val Ala Val Gly Thr Pro Asp Tyr Ile Ser Pro
225                 230                 235                 240
```

```
gag atc ctg cag gcc atg gag gag ggc aag ggc cac tac ggc cca cag   768
Glu Ile Leu Gln Ala Met Glu Glu Gly Lys Gly His Tyr Gly Pro Gln
                245                 250                 255

tgt gac tgg tgg tcg ctt gga gtc tgc gcc tat gag ctg ctc ttt ggg   816
Cys Asp Trp Trp Ser Leu Gly Val Cys Ala Tyr Glu Leu Leu Phe Gly
            260                 265                 270

gag acg ccc ttc tat gct gag tcc ttg gtg gaa acc tac ggc aag atc   864
Glu Thr Pro Phe Tyr Ala Glu Ser Leu Val Glu Thr Tyr Gly Lys Ile
        275                 280                 285

atg aac cac gag gac cac ctg cag ttc ccc ccg gac gtg cct gac gtg   912
Met Asn His Glu Asp His Leu Gln Phe Pro Pro Asp Val Pro Asp Val
    290                 295                 300

cca gcc agc gcc caa gac ctg atc cgc cag ctg ctg tgt cgc cag gaa   960
Pro Ala Ser Ala Gln Asp Leu Ile Arg Gln Leu Leu Cys Arg Gln Glu
305                 310                 315                 320

gag cgg cta ggc cgt ggt ggg ctg gat gac ttc cgg aac cat cct ttc   1008
Glu Arg Leu Gly Arg Gly Gly Leu Asp Asp Phe Arg Asn His Pro Phe
                325                 330                 335

ttc gaa ggc gtg gac tgg gag cgg ctg gcg agc agc acg gcc ccc tat   1056
Phe Glu Gly Val Asp Trp Glu Arg Leu Ala Ser Ser Thr Ala Pro Tyr
            340                 345                 350

att cct gag ctg cgg gga ccc atg gac acc tcc aac ttt gat gtg gat   1104
Ile Pro Glu Leu Arg Gly Pro Met Asp Thr Ser Asn Phe Asp Val Asp
        355                 360                 365

gac gac acc ctc aac cat cca gtg agt ggc aaa ggc cac tgc agg agg   1152
Asp Asp Thr Leu Asn His Pro Val Ser Gly Lys Gly His Cys Arg Arg
    370                 375                 380

gga gct gcc cta ccc cct tgt ttc tac caa caa aca tgg ccc ctg tcc   1200
Gly Ala Ala Leu Pro Pro Cys Phe Tyr Gln Gln Thr Trp Pro Leu Ser
385                 390                 395                 400

ccc tac agt cac agt cct gag agc agc tct gag gct tgg gct gcc ctg   1248
Pro Tyr Ser His Ser Pro Glu Ser Ser Ser Glu Ala Trp Ala Ala Leu
                405                 410                 415

gag cgg aag ctc cag tgt ctg gag cag gag aag gtg gag ctg agc agg   1296
Glu Arg Lys Leu Gln Cys Leu Glu Gln Glu Lys Val Glu Leu Ser Arg
            420                 425                 430

aag cac caa ggt act ggg agc ggc tgg gcc ggg cct ggg tgt gct ggc   1344
Lys His Gln Gly Thr Gly Ser Gly Trp Ala Gly Pro Gly Cys Ala Gly
        435                 440                 445

cct agg ggc tgc tgc tgc ggg aat gga gga gtg gac tca cct gtg ggt   1392
Pro Arg Gly Cys Cys Cys Gly Asn Gly Gly Val Asp Ser Pro Val Gly
    450                 455                 460

acc acc tcc cct cca gag gcc ctg cac gcc ccc aca gac cat cgg gag   1440
Thr Thr Ser Pro Pro Glu Ala Leu His Ala Pro Thr Asp His Arg Glu
465                 470                 475                 480
```

```
ctg gag cag cta cgg aag gaa gtg cag act ctg cgg gac agg ctg cca   1488
Leu Glu Gln Leu Arg Lys Glu Val Gln Thr Leu Arg Asp Arg Leu Pro
                485                 490                 495

ggt atc cct tcc gcc cac ccc ccc ccc ccc ccc ccc ggg gct gag tcc   1536
Gly Ile Pro Ser Ala His Pro Pro Pro Pro Pro Pro Gly Ala Glu Ser
            500                 505                 510

cac ctg ggc tcg ggt cct gcc ctg ccc tgg aca agc tgt atg atc ctg   1584
His Leu Gly Ser Gly Pro Ala Leu Pro Trp Thr Ser Cys Met Ile Leu
        515                 520                 525

gga gag cat ttt ata ctc tct gag ccc gcg tgt ggg aaa cag gcc aag   1632
Gly Glu His Phe Ile Leu Ser Glu Pro Ala Cys Gly Lys Gln Ala Lys
    530                 535                 540

gag act tgc tcc tgg gct gag agg ctg ggg ccg cca gca ctc gag ggg   1680
Glu Thr Cys Ser Trp Ala Glu Arg Leu Gly Pro Pro Ala Leu Glu Gly
545                 550                 555                 560

cag cag gag gag ctg ctt cag agg cta cag gag gcc cag gag aga gag   1728
Gln Gln Glu Glu Leu Leu Gln Arg Leu Gln Glu Ala Gln Glu Arg Glu
                565                 570                 575

gcg gcc aca gct agc cag acc cgg gcc ctg agc tcc cag ctg gag gaa   1776
Ala Ala Thr Ala Ser Gln Thr Arg Ala Leu Ser Ser Gln Leu Glu Glu
            580                 585                 590

gcc cgg gct gcc cag agg gag gcg cgg cga ctg cag aag atg gag gcc   1824
Ala Arg Ala Ala Gln Arg Glu Ala Arg Arg Leu Gln Lys Met Glu Ala
        595                 600                 605

tcg gcc agg ctg gag ctg cag tca gcg ctg gag gcc gag atc cgc gcc   1872
Ser Ala Arg Leu Glu Leu Gln Ser Ala Leu Glu Ala Glu Ile Arg Ala
    610                 615                 620

aag cag ggc ctg cag gag cgg ctg aca cag gtg cag gag gcc cag ctg   1920
Lys Gln Gly Leu Gln Glu Arg Leu Thr Gln Val Gln Glu Ala Gln Leu
625                 630                 635                 640

cag gct gag cgg gtg agt gcc tgg gat gag atg gag cag cca cca tcc   1968
Gln Ala Glu Arg Val Ser Ala Trp Asp Glu Met Glu Gln Pro Pro Ser
                645                 650                 655

acc tcc cca tgc tgt ccc agc tct ggc cac tgt ccc ccc act tca tac   2016
Thr Ser Pro Cys Cys Pro Ser Ser Gly His Cys Pro Pro Thr Ser Tyr
            660                 665                 670

tgc cct ctt ggg cca gcc cac aac cac agc acg ctt tcc aca gcg agg   2064
Cys Pro Leu Gly Pro Ala His Asn His Ser Thr Leu Ser Thr Ala Arg
        675                 680                 685

ggg agc ggg aac gct ggc tgc agg tgc tgg gtg agc tgc agc ggc tgc   2112
Gly Ser Gly Asn Ala Gly Cys Arg Cys Trp Val Ser Cys Ser Gly Cys
    690                 695                 700

tgc tgg acg cgc ggc caa gac ccc ggc ccg tgt aca cac tca agg agg   2160
Cys Trp Thr Arg Gly Gln Asp Pro Gly Pro Cys Thr His Ser Arg Arg
705                 710                 715                 720
```

```
ctt acg aca acg ggc tgc cgc tgc tgc ctc aca cgc tct gcg ctg cca   2208
Leu Thr Thr Thr Gly Cys Arg Cys Cys Leu Thr Arg Ser Ala Leu Pro
                725                 730                 735

tcc tcg gtg agc tgg tgg agg gga ctg gag gaa gca gtc cag gcc tgc   2256
Ser Ser Val Ser Trp Trp Arg Gly Leu Glu Glu Ala Val Gln Ala Cys
            740                 745                 750

ggg agt gct ggg ctg gaa gag agg ggc aga gtg tcc ttc agc cag acc   2304
Gly Ser Ala Gly Leu Glu Glu Arg Gly Arg Val Ser Phe Ser Gln Thr
        755                 760                 765

aac gtt act cag ggc tcc tcc cag ctt tct ccc tct tac ccc gtc ccc   2352
Asn Val Thr Gln Gly Ser Ser Gln Leu Ser Pro Ser Tyr Pro Val Pro
    770                 775                 780

agc cac cct ggt ctc act cat tgc agc ctt gat ctc ctg ggc tca agt   2400
Ser His Pro Gly Leu Thr His Cys Ser Leu Asp Leu Leu Gly Ser Ser
785                 790                 795                 800

aat cct cct gct tca gcc tct tgt gaa aag caa aga cga agc gaa cca   2448
Asn Pro Pro Ala Ser Ala Ser Cys Glu Lys Gln Arg Arg Ser Glu Pro
                805                 810                 815

tct ctc tcc att gtg                                             2463
Ser Leu Ser Ile Val
            820
```

<210> 8
<211> 821
<212> PRT
<213> Homo sapiens

<400> 8

```
Met Glu Arg Arg Leu Arg Ala Leu Glu Gln Leu Ala Arg Gly Glu Ala
 1               5                  10                  15
Gly Gly Cys Pro Gly Leu Asp Gly Leu Leu Asp Leu Leu Leu Ala Leu
            20                  25                  30
His His Glu Leu Ser Ser Gly Pro Leu Arg Arg Glu Arg Ser Val Ala
        35                  40                  45
Gln Phe Leu Ser Trp Ala Ser Pro Phe Val Ser Lys Val Lys Glu Leu
    50                  55                  60
Arg Leu Gln Arg Asp Asp Phe Glu Ile Leu Lys Val Ile Gly Arg Gly
65                  70                  75                  80
Ala Phe Gly Glu Val Thr Val Val Arg Gln Arg Asp Thr Gly Gln Ile
                85                  90                  95
Phe Ala Met Lys Met Leu His Lys Trp Glu Met Leu Lys Arg Ala Glu
            100                 105                 110
Val Thr Cys Phe Arg Glu Glu Arg Asp Val Leu Val Lys Gly Asp Ser
        115                 120                 125
Arg Trp Val Thr Thr Leu His Tyr Ala Phe Gln Asp Glu Glu Tyr Leu
    130                 135                 140
Tyr Leu Val Met Asp Tyr Tyr Ala Gly Gly Asp Leu Leu Thr Leu Leu
145                 150                 155                 160
Ser Arg Phe Glu Asp Arg Leu Pro Pro Glu Leu Ala Gln Phe Tyr Leu
                165                 170                 175
Ala Glu Met Val Leu Ala Ile His Ser Leu His Gln Leu Gly Tyr Val
            180                 185                 190
His Arg Asp Val Lys Pro Asp Asn Val Leu Leu Asp Val Asn Gly His
        195                 200                 205
```

```
Ile Arg Leu Ala Asp Phe Gly Ser Cys Leu Arg Leu Asn Thr Asn Gly
    210                 215                 220
Met Val Asp Ser Ser Val Ala Val Gly Thr Pro Asp Tyr Ile Ser Pro
225                 230                 235                 240
Glu Ile Leu Gln Ala Met Glu Glu Gly Lys Gly His Tyr Gly Pro Gln
                245                 250                 255
Cys Asp Trp Trp Ser Leu Gly Val Cys Ala Tyr Glu Leu Leu Phe Gly
            260                 265                 270
Glu Thr Pro Phe Tyr Ala Glu Ser Leu Val Glu Thr Tyr Gly Lys Ile
        275                 280                 285
Met Asn His Glu Asp His Leu Gln Phe Pro Pro Asp Val Pro Asp Val
    290                 295                 300
Pro Ala Ser Ala Gln Asp Leu Ile Arg Gln Leu Leu Cys Arg Gln Glu
305                 310                 315                 320
Glu Arg Leu Gly Arg Gly Gly Leu Asp Asp Phe Arg Asn His Pro Phe
                325                 330                 335
Phe Glu Gly Val Asp Trp Glu Arg Leu Ala Ser Ser Thr Ala Pro Tyr
            340                 345                 350
Ile Pro Glu Leu Arg Gly Pro Met Asp Thr Ser Asn Phe Asp Val Asp
        355                 360                 365
Asp Asp Thr Leu Asn His Pro Val Ser Gly Lys Gly His Cys Arg Arg
    370                 375                 380
Gly Ala Ala Leu Pro Pro Cys Phe Tyr Gln Gln Thr Trp Pro Leu Ser
385                 390                 395                 400
Pro Tyr Ser His Ser Pro Glu Ser Ser Ser Glu Ala Trp Ala Ala Leu
                405                 410                 415
Glu Arg Lys Leu Gln Cys Leu Glu Gln Glu Lys Val Glu Leu Ser Arg
            420                 425                 430
Lys His Gln Gly Thr Gly Ser Gly Trp Ala Gly Pro Gly Cys Ala Gly
        435                 440                 445
Pro Arg Gly Cys Cys Cys Gly Asn Gly Gly Val Asp Ser Pro Val Gly
    450                 455                 460
Thr Thr Ser Pro Pro Glu Ala Leu His Ala Pro Thr Asp His Arg Glu
465                 470                 475                 480
Leu Glu Gln Leu Arg Lys Glu Val Gln Thr Leu Arg Asp Arg Leu Pro
                485                 490                 495
Gly Ile Pro Ser Ala His Pro Pro Pro Pro Pro Pro Gly Ala Glu Ser
            500                 505                 510
His Leu Gly Ser Gly Pro Ala Leu Pro Trp Thr Ser Cys Met Ile Leu
        515                 520                 525
Gly Glu His Phe Ile Leu Ser Glu Pro Ala Cys Gly Lys Gln Ala Lys
    530                 535                 540
Glu Thr Cys Ser Trp Ala Glu Arg Leu Gly Pro Pro Ala Leu Glu Gly
545                 550                 555                 560
Gln Gln Glu Glu Leu Leu Gln Arg Leu Gln Glu Ala Gln Glu Arg Glu
                565                 570                 575
Ala Ala Thr Ala Ser Gln Thr Arg Ala Leu Ser Ser Gln Leu Glu Glu
            580                 585                 590
Ala Arg Ala Ala Gln Arg Glu Ala Arg Arg Leu Gln Lys Met Glu Ala
        595                 600                 605
Ser Ala Arg Leu Glu Leu Gln Ser Ala Leu Glu Ala Glu Ile Arg Ala
    610                 615                 620
Lys Gln Gly Leu Gln Glu Arg Leu Thr Gln Val Gln Glu Ala Gln Leu
625                 630                 635                 640
Gln Ala Glu Arg Val Ser Ala Trp Asp Glu Met Glu Gln Pro Pro Ser
                645                 650                 655
Thr Ser Pro Cys Cys Pro Ser Ser Gly His Cys Pro Pro Thr Ser Tyr
            660                 665                 670
Cys Pro Leu Gly Pro Ala His Asn His Ser Thr Leu Ser Thr Ala Arg
        675                 680                 685
Gly Ser Gly Asn Ala Gly Cys Arg Cys Trp Val Ser Cys Ser Gly Cys
    690                 695                 700
```

```
Cys Trp Thr Arg Gly Gln Asp Pro Gly Pro Cys Thr His Ser Arg Arg
705                 710                 715                 720
Leu Thr Thr Thr Gly Cys Arg Cys Cys Leu Thr Arg Ser Ala Leu Pro
                725                 730                 735
Ser Ser Val Ser Trp Trp Arg Gly Leu Glu Glu Ala Val Gln Ala Cys
            740                 745                 750
Gly Ser Ala Gly Leu Glu Glu Arg Gly Arg Val Ser Phe Ser Gln Thr
        755                 760                 765
Asn Val Thr Gln Gly Ser Ser Gln Leu Ser Pro Ser Tyr Pro Val Pro
    770                 775                 780
Ser His Pro Gly Leu Thr His Cys Ser Leu Asp Leu Leu Gly Ser Ser
785                 790                 795                 800
Asn Pro Pro Ala Ser Ala Ser Cys Glu Lys Gln Arg Arg Ser Glu Pro
                805                 810                 815
Ser Leu Ser Ile Val
            820
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<210> 9
<211> 840
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(840)
<223> MOOSE03177

<400> 9

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ctg gaa aca tac gtg aaa ctg gac aaa ctg gga gag ggc acc tat gcc   48
Leu Glu Thr Tyr Val Lys Leu Asp Lys Leu Gly Glu Gly Thr Tyr Ala
 1               5                  10                  15

aca gtc ttc aaa ggg cgc agc aaa ctg acg gag aac ctt gtg gcc ctg   96
Thr Val Phe Lys Gly Arg Ser Lys Leu Thr Glu Asn Leu Val Ala Leu
            20                  25                  30

aaa gag atc cgg ctg gag cac gag gag gga gcg ccc tgc act gcc atc   144
Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr Ala Ile
        35                  40                  45

cga gag gtg tct ctg ctg aag aac ctg aag cac gcc aat att gtg acc   192
Arg Glu Val Ser Leu Leu Lys Asn Leu Lys His Ala Asn Ile Val Thr
    50                  55                  60

ctg cat gac ctc atc cac aca gat cgg tcc ctc acc ctg gtg ttt gag   240
Leu His Asp Leu Ile His Thr Asp Arg Ser Leu Thr Leu Val Phe Glu
65                  70                  75                  80

tac ctg gtg aga gac agt gac ctg aag cag tat ctg gac cac tgt ggg   288
Tyr Leu Val Arg Asp Ser Asp Leu Lys Gln Tyr Leu Asp His Cys Gly
                85                  90                  95

aac ctc atg agc atg cac aac gtc aag att ttc atg ttc cag ctg ctc   336
Asn Leu Met Ser Met His Asn Val Lys Ile Phe Met Phe Gln Leu Leu
            100                 105                 110

cgg ggc ctc gcc tac tgt cac cac cgc aag atc ctg cac cgg gag ctg   384
Arg Gly Leu Ala Tyr Cys His His Arg Lys Ile Leu His Arg Glu Leu
        115                 120                 125
```

```
aag ccc cag aac ctg ctc atc aac gag agg ggg gag ctg aag ctg gcc   432
Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
    130                 135                 140

gac ttt gga ctg gcc agg gcc aag tca gtg ccc aca aag act tac tcc   480
Asp Phe Gly Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser
145                 150                 155                 160

aat gag gtg gtg acc ctg tgg tac agg ccc ccc gat gtg ctg ctg gga   528
Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly
                165                 170                 175

tcc aca gag tac tcc acc ccc att gat atg tgg tcc tgt gga tgc atc   576
Ser Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp Ser Cys Gly Cys Ile
            180                 185                 190

agg tgt tgc atg ttt gag gaa ctg aag aca gcc cag act gaa tat ctg   624
Arg Cys Cys Met Phe Glu Glu Leu Lys Thr Ala Gln Thr Glu Tyr Leu
        195                 200                 205

aat gga aat ggg gta ccg gag cag ctg gac tca tca agc tgg aaa tcc   672
Asn Gly Asn Gly Val Pro Glu Gln Leu Asp Ser Ser Ser Trp Lys Ser
    210                 215                 220

atg caa caa atg cca gga att aag aaa gag gca ctg aaa agg gaa aaa   720
Met Gln Gln Met Pro Gly Ile Lys Lys Glu Ala Leu Lys Arg Glu Lys
225                 230                 235                 240

gaa aaa tcc aca aaa ctg aac act ctg gaa tgc aca cat ttc agc cca   768
Glu Lys Ser Thr Lys Leu Asn Thr Leu Glu Cys Thr His Phe Ser Pro
                245                 250                 255

gct ctc cgt aga tgt gtg cag tgc att gca caa agc ttt ctg cag act   816
Ala Leu Arg Arg Cys Val Gln Cys Ile Ala Gln Ser Phe Leu Gln Thr
            260                 265                 270

aga aaa tcc atg ttt gtg gaa cat                                  840
Arg Lys Ser Met Phe Val Glu His
        275                 280
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<210> 10
<211> 280
<212> PRT
<213> Homo sapiens

<400> 10

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Leu Glu Thr Tyr Val Lys Leu Asp Lys Leu Gly Glu Gly Thr Tyr Ala
 1               5                  10                  15
Thr Val Phe Lys Gly Arg Ser Lys Leu Thr Glu Asn Leu Val Ala Leu
            20                  25                  30
Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr Ala Ile
        35                  40                  45
Arg Glu Val Ser Leu Leu Lys Asn Leu Lys His Ala Asn Ile Val Thr
    50                  55                  60
Leu His Asp Leu Ile His Thr Asp Arg Ser Leu Thr Leu Val Phe Glu
65                  70                  75                  80
Tyr Leu Val Arg Asp Ser Asp Leu Lys Gln Tyr Leu Asp His Cys Gly
                85                  90                  95
Asn Leu Met Ser Met His Asn Val Lys Ile Phe Met Phe Gln Leu Leu
            100                 105                 110
```

```
Arg Gly Leu Ala Tyr Cys His His Arg Lys Ile Leu His Arg Glu Leu
        115                 120                 125
Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
    130                 135                 140
Asp Phe Gly Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser
145                 150                 155                 160
Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly
                165                 170                 175
Ser Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp Ser Cys Gly Cys Ile
            180                 185                 190
Arg Cys Cys Met Phe Glu Glu Leu Lys Thr Ala Gln Thr Glu Tyr Leu
        195                 200                 205
Asn Gly Asn Gly Val Pro Glu Gln Leu Asp Ser Ser Ser Trp Lys Ser
    210                 215                 220
Met Gln Gln Met Pro Gly Ile Lys Lys Glu Ala Leu Lys Arg Glu Lys
225                 230                 235                 240
Glu Lys Ser Thr Lys Leu Asn Thr Leu Glu Cys Thr His Phe Ser Pro
                245                 250                 255
Ala Leu Arg Arg Cys Val Gln Cys Ile Ala Gln Ser Phe Leu Gln Thr
            260                 265                 270
Arg Lys Ser Met Phe Val Glu His
        275                 280
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<210> 11
<211> 1125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1125)
<223> MOOSE03219

<400> 11

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atg gcg gcg gcg gcg gct cag ggg ggc ggg ggc ggg gag ccc cgt aga   48
Met Ala Ala Ala Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg
 1               5                  10                  15

acc gag ggg gtc ggc ccg ggg gtc ccg ggg gag gtg gag atg gtg aag   96
Thr Glu Gly Val Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys
            20                  25                  30

ggg cag ccg ttc gac gtg ggc ccg cgc tac acg cag cca cag cag cag   144
Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Pro Gln Gln Gln
        35                  40                  45

cct ctc tcc ggt ccc ctc agc tcg gcc tat gac cac gtg cgc aag act   192
Pro Leu Ser Gly Pro Leu Ser Ser Ala Tyr Asp His Val Arg Lys Thr
    50                  55                  60

cgc gtg gcc atc aag aag atc agc ccc ttc gaa cat cag acc tac tgc   240
Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys
65                  70                  75                  80

cag cgc acg ctc cgg gag atc cag atc ctg ctg cgc ttc cgc cat gag   288
Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu
                85                  90                  95

aat gtc atc ggc atc cga gac att ctg cgg gcg tcc acc ctg gaa gcc   336
Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala
            100                 105                 110
```

```
atg aga gat gtc tac att gtg cag gac ctg atg gag act gac ctg tac   384
Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr
        115                 120                 125

aag ttg ctg aaa agc cag cag ctg agc aat gac cat atc tgc tac ttc   432
Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe
    130                 135                 140

ctc tac cag atc ctg cgg ggc ctc aag tac atc cac tcc gcc aac gtg   480
Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val
145                 150                 155                 160

ctc cac cga gat cta aag ccc tcc aac ctg ctc atc aac acc acc tgc   528
Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn Thr Thr Cys
                165                 170                 175

gac ctt aag att tgt gat ttc ggc ctg gcc cgg att gcc gat cct gag   576
Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu
            180                 185                 190

cat gac cac acc ggc ttc ctg acg gag tat gtg gct acg cgc tgg tac   624
His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr
        195                 200                 205

cgg gcc cca gag atc atg ctg aac tcc aag ggc tat acc aag tcc atc   672
Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile
    210                 215                 220

gac atc tgg tct gtg ggc tgc att ctg gct gag atg ctc tct aac cgg   720
Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg
225                 230                 235                 240

ccc atc ttc cct ggc aag cac tac ctg gat cag ctc aac cac att ctg   768
Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu
                245                 250                 255

ggc atc ctg ggc tcc cca tcc cag gag gac ctg aat tgt atc atc aac   816
Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn
            260                 265                 270

atg aag gcc cga aac tac cta cag tct ctg ccc tcc aag acc aag gtg   864
Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val
        275                 280                 285

gct tgg gcc aag ctt ttc ccc aag tca gac tcc aaa gcc ctt gac ctg   912
Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu
    290                 295                 300

ctg gac cgg atg tta acc ttt aac ccc aat aaa cgg atc aca gtg gag   960
Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu
305                 310                 315                 320

gaa gcg ctg gct cac ccc tac ctg gag cag tac tat gac ccg acg gat   1008
Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp
                325                 330                 335

gag cca gtg gcc gag gag ccc ttc acc ttc gcc atg gag ctg gat gac   1056
Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp
            340                 345                 350
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cta cct aag gag cgg ctg aag gag ctc atc ttc cag gag aca gca cgc   1104
Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg
        355                 360                 365

ttc cag ccc gga gtg ctg gag                                     1125
Phe Gln Pro Gly Val Leu Glu
    370                 375


<210> 12
<211> 375
<212> PRT
<213> Homo sapiens

<400> 12
Met Ala Ala Ala Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg
 1               5                  10                  15
Thr Glu Gly Val Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys
            20                  25                  30
Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Pro Gln Gln Gln
        35                  40                  45
Pro Leu Ser Gly Pro Leu Ser Ser Ala Tyr Asp His Val Arg Lys Thr
    50                  55                  60
Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys
65                  70                  75                  80
Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu
                85                  90                  95
Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala
            100                 105                 110
Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr
        115                 120                 125
Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe
    130                 135                 140
Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val
145                 150                 155                 160
Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn Thr Thr Cys
                165                 170                 175
Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu
            180                 185                 190
His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr
        195                 200                 205
Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile
    210                 215                 220
Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg
225                 230                 235                 240
Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu
                245                 250                 255
Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn
            260                 265                 270
Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val
        275                 280                 285
Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu
    290                 295                 300
Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu
305                 310                 315                 320
Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp
                325                 330                 335
Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp
            340                 345                 350
Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg
        355                 360                 365
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Phe Gln Pro Gly Val Leu Glu
    370                 375


<210> 13
<211> 1296
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1296)
<223> MOOSE03288

<400> 13
atg tcc acc atc cag tcg gag act gac tgc tac gac atc atc gag gtc   48
Met Ser Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
 1               5                  10                  15

ttg ggc aag ggg acc ttc ggg gag gta gcc aag ggc tgg cgg cgg agc   96
Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
            20                  25                  30

acg ggc gag atg gtg gcc atc aag atc ctc aag aat gac gcc tac cgc   144
Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
        35                  40                  45

aac cgc atc atc aag aac gag ctg aag ctg ctg cac tgc atg cga ggc   192
Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
    50                  55                  60

cta gac cct gaa gag gcc cac gtc atc cgc ttc ctt gag ttc ttc cat   240
Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65                  70                  75                  80

gac gcc ctc aag ttc tac ctg gtc ttt gag ctg ctg gag caa aac ctt   288
Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
                85                  90                  95

ttc gag ttc cag aag gag aac aac ttc gcg ccc ctc ccc gcc cgc cac   336
Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
            100                 105                 110

atc cgt aca gtc acc ctg cag gtg ctc aca gcc ctg gcc cgg ctc aag   384
Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys
        115                 120                 125

gag ctg gct atc atc cac gct gat ctc aag cct gag aac atc atg ctg   432
Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
    130                 135                 140

gtg gac cag acc cgc tgc ccc ttc agg gtg att gac ttc gga tcc gcc   480
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Ile Asp Phe Gly Ser Ala
145                 150                 155                 160

agc att ttc agc gag gtg cgc tac gtg aag gag cca tac atc cag tcg   528
Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile Gln Ser
                165                 170                 175

cgc ttc tac cgg gcc cct gag atc ctg ctg ggg ctg ccc ttc tgc gag   576
Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe Cys Glu
            180                 185                 190
```

```
aag gtg gac gtg tgg tcc ctg ggc tgc gtc atg gct gag ctg cac ctg   624
Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu His Leu
        195                 200                 205

ggc tgg cct ctc tac ccc ggc aac aac gag tac gac cag gtg cgc tac   672
Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val Arg Tyr
    210                 215                 220

atc tgc gaa acc cag ggc ctg ccc aag cca cac ctg ttg cac gcc gcc   720
Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His Ala Ala
225                 230                 235                 240

tgc aag gcc cac cac ttc ttc aag cgc aac ccc cac cct gac gct gcc   768
Cys Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp Ala Ala
                245                 250                 255

aac ccc tgg cag ctc aat cgg cta acc ttc cct gac cgg gag gcg ctg   816
Asn Pro Trp Gln Leu Asn Arg Leu Thr Phe Pro Asp Arg Glu Ala Leu
            260                 265                 270

gcg gag cac gcc gac ctc aag agc atg gtg gag ctg atc aag cgc atg   864
Ala Glu His Ala Asp Leu Lys Ser Met Val Glu Leu Ile Lys Arg Met
        275                 280                 285

ctg acc tgg gag tca cac gaa cgc atc agc ccc agt gct gcc ctg cgc   912
Leu Thr Trp Glu Ser His Glu Arg Ile Ser Pro Ser Ala Ala Leu Arg
    290                 295                 300

cac ccc ttc gtg tcc atg cag cag ctg cgc agt gcc cac gag acc acc   960
His Pro Phe Val Ser Met Gln Gln Leu Arg Ser Ala His Glu Thr Thr
305                 310                 315                 320

cac tac tac cag ctc tcg ctg cgc agc tac cgc ctc tcg ctg caa gtg  1008
His Tyr Tyr Gln Leu Ser Leu Arg Ser Tyr Arg Leu Ser Leu Gln Val
                325                 330                 335

gag ggg aag ccc ccc acg ccc gtc gtg gcc gca gaa gat ggg acc ccc  1056
Glu Gly Lys Pro Pro Thr Pro Val Val Ala Ala Glu Asp Gly Thr Pro
            340                 345                 350

tac tac tgt ctg gct gag gag aag gag gct gcg gcc cct cat cct gtt  1104
Tyr Tyr Cys Leu Ala Glu Glu Lys Glu Ala Ala Ala Pro His Pro Val
        355                 360                 365

tcc agc cca tgc ctc cta cct ccc caa atc cca cat cct gca ccc ctg  1152
Ser Ser Pro Cys Leu Leu Pro Pro Gln Ile Pro His Pro Ala Pro Leu
    370                 375                 380

cct cag gct tcc tgc cct caa ccc caa tat tct gag cct tct ctt ttt  1200
Pro Gln Ala Ser Cys Pro Gln Pro Gln Tyr Ser Glu Pro Ser Leu Phe
385                 390                 395                 400

ttt tgt tgt ttt ttt gag aca gaa caa act gct atg aat att ctt gta  1248
Phe Cys Cys Phe Phe Glu Thr Glu Gln Thr Ala Met Asn Ile Leu Val
                405                 410                 415

cgt gtc tcc tgg tgt gtg caa caa gcc aca tct cat cga ttc caa gac  1296
Arg Val Ser Trp Cys Val Gln Gln Ala Thr Ser His Arg Phe Gln Asp
            420                 425                 430
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<210> 14
<211> 432
<212> PRT
<213> Homo sapiens

<400> 14
Met Ser Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
1 5 10 15
Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
20 25 30
Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
35 40 45
Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
50 55 60
Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65 70 75 80
Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
85 90 95
Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
100 105 110
Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys
115 120 125
Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Ile Asp Phe Gly Ser Ala
145 150 155 160
Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile Gln Ser
165 170 175
Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe Cys Glu
180 185 190
Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu His Leu
195 200 205
Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val Arg Tyr
210 215 220
Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His Ala Ala
225 230 235 240
Cys Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp Ala Ala
245 250 255
Asn Pro Trp Gln Leu Asn Arg Leu Thr Phe Pro Asp Arg Glu Ala Leu
260 265 270
Ala Glu His Ala Asp Leu Lys Ser Met Val Glu Leu Ile Lys Arg Met
275 280 285
Leu Thr Trp Glu Ser His Glu Arg Ile Ser Pro Ser Ala Ala Leu Arg
290 295 300
His Pro Phe Val Ser Met Gln Gln Leu Arg Ser Ala His Glu Thr Thr
305 310 315 320
His Tyr Tyr Gln Leu Ser Leu Arg Ser Tyr Arg Leu Ser Leu Gln Val
325 330 335
Glu Gly Lys Pro Pro Thr Pro Val Val Ala Ala Glu Asp Gly Thr Pro
340 345 350
Tyr Tyr Cys Leu Ala Glu Glu Lys Glu Ala Ala Ala Pro His Pro Val
355 360 365
Ser Ser Pro Cys Leu Leu Pro Pro Gln Ile Pro His Pro Ala Pro Leu
370 375 380
Pro Gln Ala Ser Cys Pro Gln Pro Gln Tyr Ser Glu Pro Ser Leu Phe
385 390 395 400
Phe Cys Cys Phe Phe Glu Thr Glu Gln Thr Ala Met Asn Ile Leu Val
405 410 415
Arg Val Ser Trp Cys Val Gln Gln Ala Thr Ser His Arg Phe Gln Asp
420 425 430

<210> 15
<211> 1383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1383)
<223> MOOSE03296

<400> 15

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cat tgt gcc aca ctg gaa cag tgg ccc tct agc tac aag aca aga ggt   48
His Cys Ala Thr Leu Glu Gln Trp Pro Ser Ser Tyr Lys Thr Arg Gly
 1               5                  10                  15

cag aga aga ggc att cga act aaa aga atg aaa ttg aaa tgt tcc caa   96
Gln Arg Arg Gly Ile Arg Thr Lys Arg Met Lys Leu Lys Cys Ser Gln
            20                  25                  30

cac aaa aaa atg ata aat gtt gac aaa aaa aaa aaa aaa tcc agg aaa   144
His Lys Lys Met Ile Asn Val Asp Lys Lys Lys Lys Lys Ser Arg Lys
        35                  40                  45

aaa aat cac cag aaa cta gaa cgt gag gct cgg ata tgt cga ctt ctg   192
Lys Asn His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu
    50                  55                  60

aaa cat cca aac atc gtg cgc ctc cat gac agt att tct gaa gaa ggg   240
Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly
65                  70                  75                  80

ttt cac tac ctc gtg ttt gac ctt gtt acc ggc ggg gag ctg ttt gaa   288
Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu
                85                  90                  95

gac att gtg gcc aga gag tac tac agt gaa gca gat gcc agc cac tgt   336
Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys
            100                 105                 110

ata cat cag att ctg gag agt gtt aac cac atc cac cag cat gac atc   384
Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile
        115                 120                 125

gtc cac agg gac ctg aag cct gag aac ctg ctg ctg gcg agt aaa tgc   432
Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
    130                 135                 140

aag ggt gcc gcc gtc aag ctg gct gat ttt ggc cta gcc atc gaa gta   480
Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
145                 150                 155                 160

cag gga gag cag cag gct tgg ttt ggt aag ggt ttt gct ggc acc cca   528
Gln Gly Glu Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro
                165                 170                 175

ggt tac ttg tcc cct gag gtc ttg agg aaa gat ccc tat gga aaa cct   576
Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro
            180                 185                 190

gtg gat atc tgg gcc tgc ggg gtc atc ctg tat atc ctc ctg gtg ggc   624
Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly
        195                 200                 205
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```
tat cct ccc ttc tgg gat gag gat cag cac aag ctg tat cag cag atc   672
Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile
    210                 215                 220

aag gct gga gcc tat gat ttc cca tca cca gaa tgg gac acg gta act   720
Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr
225                 230                 235                 240

cct gaa gcc aag aac ttg atc aac cag atg ctg acc ata aac cca gca   768
Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala
                245                 250                 255

aag cgc atc acg gct gac cag gct ctc aag cac ccg tgg gtc tgt caa   816
Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln
            260                 265                 270

cga tcc acg gtg gca tcc atg atg cat cgt cag gag act gtg gag tgt   864
Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys
        275                 280                 285

ttg cgc aag ttc aat gcc cgg aga aaa ctg aag ggt gcc atc ctc acg   912
Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr
    290                 295                 300

acc atg ctt gtc tcc agg aac ttc tca ggt att cgg aag ggt aat ctt   960
Thr Met Leu Val Ser Arg Asn Phe Ser Gly Ile Arg Lys Gly Asn Leu
305                 310                 315                 320

cat ctt ctc tca cag gag cca caa acc act gtg gta cac aac gct aca  1008
His Leu Leu Ser Gln Glu Pro Gln Thr Thr Val Val His Asn Ala Thr
                325                 330                 335

gat ggg atc aag ggc tcc aca gag agc tgc aac acc acc aca gaa gat  1056
Asp Gly Ile Lys Gly Ser Thr Glu Ser Cys Asn Thr Thr Thr Glu Asp
            340                 345                 350

gag gac ctc aaa gtg cga aaa cag gag atc att aag att aca gaa cag  1104
Glu Asp Leu Lys Val Arg Lys Gln Glu Ile Ile Lys Ile Thr Glu Gln
        355                 360                 365

ctg att gaa gcc atc aac aat ggg gac ttt gag gcc tac acg aag att  1152
Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu Ala Tyr Thr Lys Ile
    370                 375                 380

tgt gat cca ggc ctc act tcc ttt gag cct gag gcc ctt ggt aac ctc  1200
Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu
385                 390                 395                 400

gtg gag ggg atg gat ttc cat aag ttt tac ttt gag aat ctc ctg tcc  1248
Val Glu Gly Met Asp Phe His Lys Phe Tyr Phe Glu Asn Leu Leu Ser
                405                 410                 415

aag aac agc aag cct atc cat acc acc atc cta aac cca cac gtc cac  1296
Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His
            420                 425                 430

gtg att ggg gag gac gca gcg tgc atc gcc tac atc cgc ctc acc cag  1344
Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln
        435                 440                 445
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```
tac atc gac ggg cag ggt cgg cct cgc acc agc cag tca                1383
Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser
    450                 455                 460
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<210> 16
<211> 461
<212> PRT
<213> Homo sapiens

<400> 16

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His Cys Ala Thr Leu Glu Gln Trp Pro Ser Ser Tyr Lys Thr Arg Gly
 1               5                  10                  15
Gln Arg Arg Gly Ile Arg Thr Lys Arg Met Lys Leu Lys Cys Ser Gln
            20                  25                  30
His Lys Lys Met Ile Asn Val Asp Lys Lys Lys Lys Lys Ser Arg Lys
        35                  40                  45
Lys Asn His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu
    50                  55                  60
Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly
65                  70                  75                  80
Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu
                85                  90                  95
Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys
            100                 105                 110
Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile
        115                 120                 125
Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
    130                 135                 140
Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
145                 150                 155                 160
Gln Gly Glu Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro
                165                 170                 175
Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro
            180                 185                 190
Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly
        195                 200                 205
Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile
    210                 215                 220
Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr
225                 230                 235                 240
Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala
                245                 250                 255
Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln
            260                 265                 270
Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys
        275                 280                 285
Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr
    290                 295                 300
Thr Met Leu Val Ser Arg Asn Phe Ser Gly Ile Arg Lys Gly Asn Leu
305                 310                 315                 320
His Leu Leu Ser Gln Glu Pro Gln Thr Thr Val Val His Asn Ala Thr
                325                 330                 335
Asp Gly Ile Lys Gly Ser Thr Glu Ser Cys Asn Thr Thr Thr Glu Asp
            340                 345                 350
Glu Asp Leu Lys Val Arg Lys Gln Glu Ile Ile Lys Ile Thr Glu Gln
        355                 360                 365
Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu Ala Tyr Thr Lys Ile
    370                 375                 380
Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu
385                 390                 395                 400
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Val Glu Gly Met Asp Phe His Lys Phe Tyr Phe Glu Asn Leu Leu Ser
                405                 410                 415
Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His
            420                 425                 430
Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln
        435                 440                 445
Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser
    450                 455                 460
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<210> 17
<211> 1107
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1107)
<223> MOOSE03301

<400> 17

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agc ctt acc tta ctt tct caa gaa gag cag cta gta ctc tac cga ttc   48
Ser Leu Thr Leu Leu Ser Gln Glu Glu Gln Leu Val Leu Tyr Arg Phe
 1               5                  10                  15

tcc aga ggg gct ttt tgg aaa tat cta gaa agg aga gag aaa ata gaa   96
Ser Arg Gly Ala Phe Trp Lys Tyr Leu Glu Arg Arg Glu Lys Ile Glu
            20                  25                  30

aca aaa aaa att ttt aag tgc aaa gtt aag ctt gaa aga aaa tat cac   144
Thr Lys Lys Ile Phe Lys Cys Lys Val Lys Leu Glu Arg Lys Tyr His
        35                  40                  45

cag aaa cta gaa cgt gag gct cgg ata tgt cga ctt ctg aaa cat cca   192
Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro
    50                  55                  60

aac atc gtg cgc ctc cat gac agt att tct gaa gaa ggg ttt cac tac   240
Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr
65                  70                  75                  80

ctc gtg ttt gac ctt gtt acc ggc ggg gag ctg ttt gaa gac att gtg   288
Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val
                85                  90                  95

gcc aga gag tac tac agt gaa gca gat gcc agc cac tgt ata cat cag   336
Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln
            100                 105                 110

att ctg gag agt gtt aac cac atc cac cag cat gac atc gtc cac agg   384
Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg
        115                 120                 125

gac ctg aag cct gag aac ctg ctg ctg gcg agt aaa tgc aag ggt gcc   432
Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala
    130                 135                 140

gcc gtc aag ctg gct gat ttt ggc cta gcc atc gaa gta cag gga gag   480
Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu
145                 150                 155                 160
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```
cag cag gct tgg ttt ggt aag ggt ttt gct ggc acc cca ggt tac ttg   528
Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro Gly Tyr Leu
                165                 170                 175

tcc cct gag gtc ttg agg aaa gat ccc tat gga aaa cct gtg gat atc   576
Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile
            180                 185                 190

tgg gcc tgc ggg gtc atc ctg tat atc ctc ctg gtg ggc tat cct ccc   624
Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro
        195                 200                 205

ttc tgg gat gag gat cag cac aag ctg tat cag cag atc aag gct gga   672
Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly
    210                 215                 220

gcc tat gat ttc cca tca cca gaa tgg gac acg gta act cct gaa gcc   720
Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala
225                 230                 235                 240

aag aac ttg atc aac cag atg ctg acc ata aac cca gca aag cgc atc   768
Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg Ile
                245                 250                 255

acg gct gac cag gct ctc aag cac ccg tgg gtc tgt caa cga tcc acg   816
Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser Thr
            260                 265                 270

gtg gca tcc atg atg cat cgt cag gag act gtg gag tgt ttg cgc aag   864
Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu Arg Lys
        275                 280                 285

ttc aat gcc cgg aga aaa ctg aag ggt gcc atc ctc acg acc atg ctt   912
Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu
    290                 295                 300

gtc tcc agg aac ttc tca ggt atg aca gag tct gtc cgg aag ctt ctg   960
Val Ser Arg Asn Phe Ser Gly Met Thr Glu Ser Val Arg Lys Leu Leu
305                 310                 315                 320

cag aaa gag gtg tct atg gat gca atc aag aag gaa ggg cac ctg tgt   1008
Gln Lys Glu Val Ser Met Asp Ala Ile Lys Lys Glu Gly His Leu Cys
                325                 330                 335

gtt tct cta ggg ctg ttt ttt gag ttg acc tcc aat agg aga tgt ggc   1056
Val Ser Leu Gly Leu Phe Phe Glu Leu Thr Ser Asn Arg Arg Cys Gly
            340                 345                 350

tta tcc tgg act cta gca gaa gct cat agg aga gag cgt act gga gaa   1104
Leu Ser Trp Thr Leu Ala Glu Ala His Arg Arg Glu Arg Thr Gly Glu
        355                 360                 365

agc                                                               1107
Ser
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<210> 18
<211> 369
<212> PRT
<213> Homo sapiens

<400> 18
Ser Leu Thr Leu Leu Ser Gln Glu Glu Gln Leu Val Leu Tyr Arg Phe
1 5 10 15
Ser Arg Gly Ala Phe Trp Lys Tyr Leu Glu Arg Arg Glu Lys Ile Glu
20 25 30
Thr Lys Lys Ile Phe Lys Cys Lys Val Lys Leu Glu Arg Lys Tyr His
35 40 45
Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro
50 55 60
Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr
65 70 75 80
Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val
85 90 95
Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln
100 105 110
Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg
115 120 125
Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala
130 135 140
Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu
145 150 155 160
Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro Gly Tyr Leu
165 170 175
Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile
180 185 190
Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro
195 200 205
Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly
210 215 220
Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala
225 230 235 240
Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg Ile
245 250 255
Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser Thr
260 265 270
Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu Arg Lys
275 280 285
Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu
290 295 300
Val Ser Arg Asn Phe Ser Gly Met Thr Glu Ser Val Arg Lys Leu Leu
305 310 315 320
Gln Lys Glu Val Ser Met Asp Ala Ile Lys Lys Glu Gly His Leu Cys
325 330 335
Val Ser Leu Gly Leu Phe Phe Glu Leu Thr Ser Asn Arg Arg Cys Gly
340 345 350
Leu Ser Trp Thr Leu Ala Glu Ala His Arg Arg Glu Arg Thr Gly Glu
355 360 365
Ser

<210> 19
<211> 1086
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1086)
<223> MOOSE03304

<400> 19

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ttt gac cca cgt gtt aca gct aag tat gac atc aag gcc cta att ggc   48
Phe Asp Pro Arg Val Thr Ala Lys Tyr Asp Ile Lys Ala Leu Ile Gly
 1               5                  10                  15

cga ggc agc ttc agc cga gtg gta cgt gta gag cac cgg gca acc cgg   96
Arg Gly Ser Phe Ser Arg Val Val Arg Val Glu His Arg Ala Thr Arg
            20                  25                  30

cag ccg tat gcc atc aag atg att gag acc aag tac cgg gag ggg cgg  144
Gln Pro Tyr Ala Ile Lys Met Ile Glu Thr Lys Tyr Arg Glu Gly Arg
        35                  40                  45

gag gtg tgt gag tcg gag ctg cgt gtg ctg cgt cgg gtg cgt cat gcc  192
Glu Val Cys Glu Ser Glu Leu Arg Val Leu Arg Arg Val Arg His Ala
    50                  55                  60

aac atc atc cag ctg gtg gag gtg ttc gag aca cag gag cgg gtg tac  240
Asn Ile Ile Gln Leu Val Glu Val Phe Glu Thr Gln Glu Arg Val Tyr
65                  70                  75                  80

atg gtg atg gag ctg gcc act ggt gga gag ctc ttt gac cgc atc att  288
Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Ile Ile
                85                  90                  95

gcc aag ggc tcc ttc acc gag cgt gac gcc acg cgg gtg ctg cag atg  336
Ala Lys Gly Ser Phe Thr Glu Arg Asp Ala Thr Arg Val Leu Gln Met
            100                 105                 110

gtg ctg gat ggc gtc cgg tat ctg cat gca ctg ggc atc aca cac cga  384
Val Leu Asp Gly Val Arg Tyr Leu His Ala Leu Gly Ile Thr His Arg
        115                 120                 125

gac ctc aaa cct gag aat ctg ctc tac tac cat ccg ggc act gac tcc  432
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Thr Asp Ser
    130                 135                 140

aag atc atc atc acc gac ttc ggc ctg gcc agt gct cgc aag aag ggt  480
Lys Ile Ile Ile Thr Asp Phe Gly Leu Ala Ser Ala Arg Lys Lys Gly
145                 150                 155                 160

gat gac tgc ttg atg aag acc acc tgt ggc acg cct gag tac att gcc  528
Asp Asp Cys Leu Met Lys Thr Thr Cys Gly Thr Pro Glu Tyr Ile Ala
                165                 170                 175

cca gaa gtc ctg gtc cgc aag cca tac acc aac tca gtg gac atg tgg  576
Pro Glu Val Leu Val Arg Lys Pro Tyr Thr Asn Ser Val Asp Met Trp
            180                 185                 190

gcg ctg ggc gtc att gcc tac atc cta ctc agt ggc acc atg ccg ttt  624
Ala Leu Gly Val Ile Ala Tyr Ile Leu Leu Ser Gly Thr Met Pro Phe
        195                 200                 205

gag gat gac aac cgt acc cgg ctg tac cgg cag atc ctc agg ggc aag  672
Glu Asp Asp Asn Arg Thr Arg Leu Tyr Arg Gln Ile Leu Arg Gly Lys
    210                 215                 220

tac agt tac tct ggg gag ccc tgg cct agt gtg tcc aac ctg gcc aag  720
Tyr Ser Tyr Ser Gly Glu Pro Trp Pro Ser Val Ser Asn Leu Ala Lys
225                 230                 235                 240
```

```
gac ttc att gac cgc ctg ctg aca gtg gac cct gga gcc cgt atg act   768
Asp Phe Ile Asp Arg Leu Leu Thr Val Asp Pro Gly Ala Arg Met Thr
                245                 250                 255

gca ctg cag gcc ctg agg cac ccg tgg gtg gtg agc atg gct gcc tct   816
Ala Leu Gln Ala Leu Arg His Pro Trp Val Val Ser Met Ala Ala Ser
            260                 265                 270

tca tcc atg aag aac ctg cac cgc tcc ata tcc cag aac ctc ctt aaa   864
Ser Ser Met Lys Asn Leu His Arg Ser Ile Ser Gln Asn Leu Leu Lys
        275                 280                 285

cgt gcc tcc tcg cgc tgc cag agc acc aaa tct gcc cag tcc acg cgt   912
Arg Ala Ser Ser Arg Cys Gln Ser Thr Lys Ser Ala Gln Ser Thr Arg
    290                 295                 300

tcc agc cgc tcc aca cgc tcc aat aag tca cgc cgt cag ggg ccc agc   960
Ser Ser Arg Ser Thr Arg Ser Asn Lys Ser Arg Arg Gln Gly Pro Ser
305                 310                 315                 320

aaa ggt ttg ttg gag aaa cgt gtc atc tct ccc cat gtg agt cct gtg   1008
Lys Gly Leu Leu Glu Lys Arg Val Ile Ser Pro His Val Ser Pro Val
                325                 330                 335

acc ctt att agc ctg gaa aac ttg gag tca caa gcc cag cat gtg cag   1056
Thr Leu Ile Ser Leu Glu Asn Leu Glu Ser Gln Ala Gln His Val Gln
            340                 345                 350

aca gaa gac gag ctt cac gtg agc agt gca                          1086
Thr Glu Asp Glu Leu His Val Ser Ser Ala
        355                 360
```

<210> 20
<211> 362
<212> PRT
<213> Homo sapiens

<400> 20

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Phe Asp Pro Arg Val Thr Ala Lys Tyr Asp Ile Lys Ala Leu Ile Gly
 1               5                  10                  15
Arg Gly Ser Phe Ser Arg Val Val Arg Val Glu His Arg Ala Thr Arg
            20                  25                  30
Gln Pro Tyr Ala Ile Lys Met Ile Glu Thr Lys Tyr Arg Glu Gly Arg
        35                  40                  45
Glu Val Cys Glu Ser Glu Leu Arg Val Leu Arg Arg Val Arg His Ala
    50                  55                  60
Asn Ile Ile Gln Leu Val Glu Val Phe Glu Thr Gln Glu Arg Val Tyr
65                  70                  75                  80
Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Ile Ile
                85                  90                  95
Ala Lys Gly Ser Phe Thr Glu Arg Asp Ala Thr Arg Val Leu Gln Met
            100                 105                 110
Val Leu Asp Gly Val Arg Tyr Leu His Ala Leu Gly Ile Thr His Arg
        115                 120                 125
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Thr Asp Ser
    130                 135                 140
Lys Ile Ile Ile Thr Asp Phe Gly Leu Ala Ser Ala Arg Lys Lys Gly
145                 150                 155                 160
Asp Asp Cys Leu Met Lys Thr Thr Cys Gly Thr Pro Glu Tyr Ile Ala
                165                 170                 175
```

```
Pro Glu Val Leu Val Arg Lys Pro Tyr Thr Asn Ser Val Asp Met Trp
            180                 185                 190
Ala Leu Gly Val Ile Ala Tyr Ile Leu Leu Ser Gly Thr Met Pro Phe
        195                 200                 205
Glu Asp Asp Asn Arg Thr Arg Leu Tyr Arg Gln Ile Leu Arg Gly Lys
    210                 215                 220
Tyr Ser Tyr Ser Gly Glu Pro Trp Pro Ser Val Ser Asn Leu Ala Lys
225                 230                 235                 240
Asp Phe Ile Asp Arg Leu Leu Thr Val Asp Pro Gly Ala Arg Met Thr
                245                 250                 255
Ala Leu Gln Ala Leu Arg His Pro Trp Val Val Ser Met Ala Ala Ser
            260                 265                 270
Ser Ser Met Lys Asn Leu His Arg Ser Ile Ser Gln Asn Leu Leu Lys
        275                 280                 285
Arg Ala Ser Ser Arg Cys Gln Ser Thr Lys Ser Ala Gln Ser Thr Arg
    290                 295                 300
Ser Ser Arg Ser Thr Arg Ser Asn Lys Ser Arg Arg Gln Gly Pro Ser
305                 310                 315                 320
Lys Gly Leu Leu Glu Lys Arg Val Ile Ser Pro His Val Ser Pro Val
                325                 330                 335
Thr Leu Ile Ser Leu Glu Asn Leu Glu Ser Gln Ala Gln His Val Gln
            340                 345                 350
Thr Glu Asp Glu Leu His Val Ser Ser Ala
        355                 360
```

<210> 21
<211> 1092
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1092)
<223> MOOSE03306

<400> 21

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aca tgt ttg gtt ttt ctt ccc aac aga tat gac atc aaa gct ctt att   48
Thr Cys Leu Val Phe Leu Pro Asn Arg Tyr Asp Ile Lys Ala Leu Ile
 1               5                  10                  15

ggg aca ggc agt ttc agc agg gtt gtc agg gta gag cag aag acc acc   96
Gly Thr Gly Ser Phe Ser Arg Val Val Arg Val Glu Gln Lys Thr Thr
            20                  25                  30

aag aaa cct ttt gca ata aaa gtg atg gaa acc aga gag agg gaa ggt   144
Lys Lys Pro Phe Ala Ile Lys Val Met Glu Thr Arg Glu Arg Glu Gly
        35                  40                  45

aga gaa gcg tgc gtg tct gag ctg agc gtc ctg cgg cgg gtt agc cat   192
Arg Glu Ala Cys Val Ser Glu Leu Ser Val Leu Arg Arg Val Ser His
    50                  55                  60

cgt tac att gtc cag ctc atg gag atc ttt gag act gag gat caa gtt   240
Arg Tyr Ile Val Gln Leu Met Glu Ile Phe Glu Thr Glu Asp Gln Val
65                  70                  75                  80

tac atg gta atg gag ctg gct acc gga ggg gag ctc ttt gat cga ctc   288
Tyr Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Leu
                85                  90                  95
```

```
att gct cag gga tcc ttt aca gag cgg gat gcc gtc agg atc ctc cag   336
Ile Ala Gln Gly Ser Phe Thr Glu Arg Asp Ala Val Arg Ile Leu Gln
            100                 105                 110

atg gtt gct gat ggg att agg tat ttg cat gcg ctg cag ata act cat   384
Met Val Ala Asp Gly Ile Arg Tyr Leu His Ala Leu Gln Ile Thr His
        115                 120                 125

agg aat cta aag cct gaa aac ctc tta tac tat cat cca ggt gaa gag   432
Arg Asn Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Glu Glu
    130                 135                 140

tcg aaa att tta att aca gat ttt ggt ttg gca tac tcc ggg aaa aaa   480
Ser Lys Ile Leu Ile Thr Asp Phe Gly Leu Ala Tyr Ser Gly Lys Lys
145                 150                 155                 160

agt ggt gac tgg aca atg aag aca ctc tgt ggg acc cca gag tac ata   528
Ser Gly Asp Trp Thr Met Lys Thr Leu Cys Gly Thr Pro Glu Tyr Ile
                165                 170                 175

gct cct gag gtt ttg cta agg aag cct tat acc agt gca gtg gac atg   576
Ala Pro Glu Val Leu Leu Arg Lys Pro Tyr Thr Ser Ala Val Asp Met
            180                 185                 190

tgg gct ctt ggt gtg atc aca tat gct tta ctt agc gga ttc ctg cct   624
Trp Ala Leu Gly Val Ile Thr Tyr Ala Leu Leu Ser Gly Phe Leu Pro
        195                 200                 205

ttt gat gat gaa agc cag aca agg ctt tac agg aag att ctg aaa ggc   672
Phe Asp Asp Glu Ser Gln Thr Arg Leu Tyr Arg Lys Ile Leu Lys Gly
    210                 215                 220

aaa tat aat tat aca gga gag cct tgg cca agc att tcc cac ttg gcg   720
Lys Tyr Asn Tyr Thr Gly Glu Pro Trp Pro Ser Ile Ser His Leu Ala
225                 230                 235                 240

aag gac ttt ata gac aaa cta ctg att ttg gag gct ggt cat cgc atg   768
Lys Asp Phe Ile Asp Lys Leu Leu Ile Leu Glu Ala Gly His Arg Met
                245                 250                 255

tca gct ggc cag gcc ctg gac cat ccc tgg gtg atc acc atg gct gca   816
Ser Ala Gly Gln Ala Leu Asp His Pro Trp Val Ile Thr Met Ala Ala
            260                 265                 270

ggg tct tcc atg aag aat ctc cag agg gcc ata tcc cga aac ctc atg   864
Gly Ser Ser Met Lys Asn Leu Gln Arg Ala Ile Ser Arg Asn Leu Met
        275                 280                 285

cag agg gcc tct ccc cac tct cag agt cct gga tct gca cag tct tct   912
Gln Arg Ala Ser Pro His Ser Gln Ser Pro Gly Ser Ala Gln Ser Ser
    290                 295                 300

aag tca cat tat tct cac aaa tcc agg cat ata gtc aaa agc aaa gga   960
Lys Ser His Tyr Ser His Lys Ser Arg His Ile Val Lys Ser Lys Gly
305                 310                 315                 320

aag gcc aac aaa agc cac aga ata tct ttg tta ttc cta gca gat ttt   1008
Lys Ala Asn Lys Ser His Arg Ile Ser Leu Leu Phe Leu Ala Asp Phe
                325                 330                 335
```

```
ttt cac aag aag att aag aat ata att gtt gtt tat atc cca gcc tat   1056
Phe His Lys Lys Ile Lys Asn Ile Ile Val Val Tyr Ile Pro Ala Tyr
            340                 345                 350

aat tta tca gaa gag aaa aac ggg aaa atg gaa tct                   1092
Asn Leu Ser Glu Glu Lys Asn Gly Lys Met Glu Ser
        355                 360
```

<210> 22
<211> 364
<212> PRT
<213> Homo sapiens

<400> 22

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Thr Cys Leu Val Phe Leu Pro Asn Arg Tyr Asp Ile Lys Ala Leu Ile
 1               5                  10                  15
Gly Thr Gly Ser Phe Ser Arg Val Val Arg Val Glu Gln Lys Thr Thr
            20                  25                  30
Lys Lys Pro Phe Ala Ile Lys Val Met Glu Thr Arg Glu Arg Glu Gly
        35                  40                  45
Arg Glu Ala Cys Val Ser Glu Leu Ser Val Leu Arg Arg Val Ser His
    50                  55                  60
Arg Tyr Ile Val Gln Leu Met Glu Ile Phe Glu Thr Glu Asp Gln Val
65                  70                  75                  80
Tyr Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Leu
                85                  90                  95
Ile Ala Gln Gly Ser Phe Thr Glu Arg Asp Ala Val Arg Ile Leu Gln
            100                 105                 110
Met Val Ala Asp Gly Ile Arg Tyr Leu His Ala Leu Gln Ile Thr His
        115                 120                 125
Arg Asn Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Glu Glu
    130                 135                 140
Ser Lys Ile Leu Ile Thr Asp Phe Gly Leu Ala Tyr Ser Gly Lys Lys
145                 150                 155                 160
Ser Gly Asp Trp Thr Met Lys Thr Leu Cys Gly Thr Pro Glu Tyr Ile
                165                 170                 175
Ala Pro Glu Val Leu Leu Arg Lys Pro Tyr Thr Ser Ala Val Asp Met
            180                 185                 190
Trp Ala Leu Gly Val Ile Thr Tyr Ala Leu Leu Ser Gly Phe Leu Pro
        195                 200                 205
Phe Asp Asp Glu Ser Gln Thr Arg Leu Tyr Arg Lys Ile Leu Lys Gly
    210                 215                 220
Lys Tyr Asn Tyr Thr Gly Glu Pro Trp Pro Ser Ile Ser His Leu Ala
225                 230                 235                 240
Lys Asp Phe Ile Asp Lys Leu Leu Ile Leu Glu Ala Gly His Arg Met
                245                 250                 255
Ser Ala Gly Gln Ala Leu Asp His Pro Trp Val Ile Thr Met Ala Ala
            260                 265                 270
Gly Ser Ser Met Lys Asn Leu Gln Arg Ala Ile Ser Arg Asn Leu Met
        275                 280                 285
Gln Arg Ala Ser Pro His Ser Gln Ser Pro Gly Ser Ala Gln Ser Ser
    290                 295                 300
Lys Ser His Tyr Ser His Lys Ser Arg His Ile Val Lys Ser Lys Gly
305                 310                 315                 320
Lys Ala Asn Lys Ser His Arg Ile Ser Leu Leu Phe Leu Ala Asp Phe
                325                 330                 335
Phe His Lys Lys Ile Lys Asn Ile Ile Val Val Tyr Ile Pro Ala Tyr
            340                 345                 350
Asn Leu Ser Glu Glu Lys Asn Gly Lys Met Glu Ser
        355                 360
```

<210> 23
<211> 1158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1158)
<223> MOOSE03309

<400> 23

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cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga   48
Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly
 1               5                  10                  15

tca gga gct ttc tca gaa gtt ttc ctg gtg aag caa aga ctg act ggg   96
Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly
            20                  25                  30

aag ctc ttt gct ctg aag tgc atc aag aag tca cct gcc ttc cgg gac   144
Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp
        35                  40                  45

agc agc ctg gag aat gag att gct gtg ttg aaa aag atc aag cat gaa   192
Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu
    50                  55                  60

aac att gtg acc ctg gag gac atc tat gag agc acc acc cac tac tac   240
Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr
65                  70                  75                  80

ctg gtc atg cag ctt gtt tct ggt ggg gag ctc ttt gac cgg atc ctg   288
Leu Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu
                85                  90                  95

gag cgg ggt gtc tac aca gag aag gat gcc agt ctg gtg atc cag cag   336
Glu Arg Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln
            100                 105                 110

gtc ttg tcg gca gtg aaa tac cta cat gag aat ggc atc gtc cac aga   384
Val Leu Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg
        115                 120                 125

gac tta aag ccc gaa aac ctg ctt tac ctt acc cct gaa gag aac tct   432
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser
    130                 135                 140

aag atc atg atc act gac ttt ggt ctg tcc aag atg gaa cag aat ggc   480
Lys Ile Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly
145                 150                 155                 160

atc atg tcc act gcc tgt ggg acc cca ggc tac gtg gct cca gaa gtg   528
Ile Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
                165                 170                 175

ctg gcc cag aaa ccc tac agc aag gct gtg gat tgc tgg tcc atc ggc   576
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
            180                 185                 190

gtc atc acc tac ata ttg ctc tgt gga tac ccc cca ttc tat gaa gaa   624
Val Ile Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu
        195                 200                 205
```

```
acg gag tct aag ctt ttc gag aag atc aag gag ggc tac tat gag ttt   672
Thr Glu Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe
    210                 215                 220

gag tct cca ttc tgg gat gac att tct gag tca gcc aag gac ttt att   720
Glu Ser Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile
225                 230                 235                 240

tgc cac ttg ctt gag aag gat ccg aac gag cgg tac acc tgt gag aag   768
Cys His Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys
                245                 250                 255

gcc ttg agt cat ccc tgg gtg caa tgt tca gta cta gtt att caa gaa   816
Ala Leu Ser His Pro Trp Val Gln Cys Ser Val Leu Val Ile Gln Glu
            260                 265                 270

aaa cct cta gac cca gct ccc ctg aga tca cca tca ccg agg cac ctg   864
Lys Pro Leu Asp Pro Ala Pro Leu Arg Ser Pro Ser Pro Arg His Leu
        275                 280                 285

tcc tgg acc aca gtg gga gag ggg aga cga tcc aga gag agg aaa aac   912
Ser Trp Thr Thr Val Gly Glu Gly Arg Arg Ser Arg Glu Arg Lys Asn
    290                 295                 300

att cgc aaa ggc aag agg caa gag aaa gtg tat ggc ggt gtt aaa gag   960
Ile Arg Lys Gly Lys Arg Gln Glu Lys Val Tyr Gly Gly Val Lys Glu
305                 310                 315                 320

gct acc caa agc ccc tca ata acc aat ccc acc cca cac ctg gga aac  1008
Ala Thr Gln Ser Pro Ser Ile Thr Asn Pro Thr Pro His Leu Gly Asn
                325                 330                 335

caa cag cca gac atc tcc atg aca acc aag cac cag aaa cag cca gac  1056
Gln Gln Pro Asp Ile Ser Met Thr Thr Lys His Gln Lys Gln Pro Asp
            340                 345                 350

atc tcc atg aga gct aag gac cag aaa ctg gtt tcc ttg gca acc act  1104
Ile Ser Met Arg Ala Lys Asp Gln Lys Leu Val Ser Leu Ala Thr Thr
        355                 360                 365

gag ctc aca gtg agc agt aca agg gtc ggg atg gct ggg gga gtg ggg  1152
Glu Leu Thr Val Ser Ser Thr Arg Val Gly Met Ala Gly Gly Val Gly
    370                 375                 380

ttc tca                                                         1158
Phe Ser
385
```

<210> 24
<211> 386
<212> PRT
<213> Homo sapiens

<400> 24

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Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly
 1               5                  10                  15
Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly
            20                  25                  30
Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp
        35                  40                  45
```

```
Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu
    50                  55                  60
Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr
65                  70                  75                  80
Leu Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu
                85                  90                  95
Glu Arg Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln
            100                 105                 110
Val Leu Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg
        115                 120                 125
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser
    130                 135                 140
Lys Ile Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly
145                 150                 155                 160
Ile Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
                165                 170                 175
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
            180                 185                 190
Val Ile Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu
        195                 200                 205
Thr Glu Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe
    210                 215                 220
Glu Ser Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile
225                 230                 235                 240
Cys His Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys
                245                 250                 255
Ala Leu Ser His Pro Trp Val Gln Cys Ser Val Leu Val Ile Gln Glu
            260                 265                 270
Lys Pro Leu Asp Pro Ala Pro Leu Arg Ser Pro Ser Pro Arg His Leu
        275                 280                 285
Ser Trp Thr Thr Val Gly Glu Gly Arg Arg Ser Arg Glu Arg Lys Asn
    290                 295                 300
Ile Arg Lys Gly Lys Arg Gln Glu Lys Val Tyr Gly Gly Val Lys Glu
305                 310                 315                 320
Ala Thr Gln Ser Pro Ser Ile Thr Asn Pro Thr Pro His Leu Gly Asn
                325                 330                 335
Gln Gln Pro Asp Ile Ser Met Thr Thr Lys His Gln Lys Gln Pro Asp
            340                 345                 350
Ile Ser Met Arg Ala Lys Asp Gln Lys Leu Val Ser Leu Ala Thr Thr
        355                 360                 365
Glu Leu Thr Val Ser Ser Thr Arg Val Gly Met Ala Gly Gly Val Gly
    370                 375                 380
Phe Ser
385


<210> 25
<211> 1260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1260)
<223> MOOSE03312

<400> 25
gaa tca tca act ctt ctt gag aaa tac aaa att gga aag gtc att ggt   48
Glu Ser Ser Thr Leu Leu Glu Lys Tyr Lys Ile Gly Lys Val Ile Gly
 1               5                  10                  15
```

```
gat ggc aat ttt gca gta gtc aaa gag tgt ata gac agg tcc act gga   96
Asp Gly Asn Phe Ala Val Val Lys Glu Cys Ile Asp Arg Ser Thr Gly
            20                  25                  30

aag gag ttt gcc cta aag att ata gac aaa gcc aaa tgt tgt gga aag   144
Lys Glu Phe Ala Leu Lys Ile Ile Asp Lys Ala Lys Cys Cys Gly Lys
        35                  40                  45

gaa cac ctg att gag aat gaa gtg tca ata ctg cgc cga gtg aaa cat   192
Glu His Leu Ile Glu Asn Glu Val Ser Ile Leu Arg Arg Val Lys His
    50                  55                  60

ccc aat atc att atg ctg gtc gag gag atg gaa aca gca act gag ctc   240
Pro Asn Ile Ile Met Leu Val Glu Glu Met Glu Thr Ala Thr Glu Leu
65                  70                  75                  80

ttt ctg gtg atg gaa ttg gtc aaa ggt gga gat ctc ttt gat gca att   288
Phe Leu Val Met Glu Leu Val Lys Gly Gly Asp Leu Phe Asp Ala Ile
                85                  90                  95

act tcg tcg acc aag tac act gag aga gat ggc agt gcc atg gtg tac   336
Thr Ser Ser Thr Lys Tyr Thr Glu Arg Asp Gly Ser Ala Met Val Tyr
            100                 105                 110

aac tta gcc aat gcc ctc agg tat ctc cat ggc ctc agc atc gtg cac   384
Asn Leu Ala Asn Ala Leu Arg Tyr Leu His Gly Leu Ser Ile Val His
        115                 120                 125

aga gac atc aaa cca gag aat ctc ttg gtg tgt gaa tat cct gat gga   432
Arg Asp Ile Lys Pro Glu Asn Leu Leu Val Cys Glu Tyr Pro Asp Gly
    130                 135                 140

acc aag tct ttg aaa ctg gga gac ttt ggg ctt gcg act gtg gta gaa   480
Thr Lys Ser Leu Lys Leu Gly Asp Phe Gly Leu Ala Thr Val Val Glu
145                 150                 155                 160

ggc cct tta tac aca gtc tgt ggc aca ccc act tat gtg gct cca gaa   528
Gly Pro Leu Tyr Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu
                165                 170                 175

atc att gct gaa act ggc tat ggc ctg aag gtg gac att tgg gca gct   576
Ile Ile Ala Glu Thr Gly Tyr Gly Leu Lys Val Asp Ile Trp Ala Ala
            180                 185                 190

ggt gtg atc aca tac ata ctt ctc tgt gga ttc cca cca ttc cga agt   624
Gly Val Ile Thr Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser
        195                 200                 205

gag aac aat ctc cag gaa gat ctc ttc gac cag atc ttg gct ggg aag   672
Glu Asn Asn Leu Gln Glu Asp Leu Phe Asp Gln Ile Leu Ala Gly Lys
    210                 215                 220

ctg gag ttt ccg gcc ccc tac tgg gat aac atc acg gac tct gcc aag   720
Leu Glu Phe Pro Ala Pro Tyr Trp Asp Asn Ile Thr Asp Ser Ala Lys
225                 230                 235                 240

gaa tta atc agt caa atg ctt cag gta aat gtt gaa gct cgg tgt acc   768
Glu Leu Ile Ser Gln Met Leu Gln Val Asn Val Glu Ala Arg Cys Thr
                245                 250                 255
```

```
gcg gga caa atc ctg agt cac ccc tgg gtg tca cca atg caa ccc tgg   816
Ala Gly Gln Ile Leu Ser His Pro Trp Val Ser Pro Met Gln Pro Trp
            260                 265                 270

gcg gga agg cca gct cac cgt gag cag gta gaa gcc agc cag cca ccc   864
Ala Gly Arg Pro Ala His Arg Glu Gln Val Glu Ala Ser Gln Pro Pro
        275                 280                 285

agg cag gga cct tgg ttc tcc cca cac act ccc agg agc agg gaa cag   912
Arg Gln Gly Pro Trp Phe Ser Pro His Thr Pro Arg Ser Arg Glu Gln
    290                 295                 300

ggg tgg agt ggc ctt tcc cag agc tgg agt tgg ctg cag cag ctt tcg   960
Gly Trp Ser Gly Leu Ser Gln Ser Trp Ser Trp Leu Gln Gln Leu Ser
305                 310                 315                 320

aat cag acc tgc caa ggt gat ggg cgt ctg agt ttc aca tct ggg ccc   1008
Asn Gln Thr Cys Gln Gly Asp Gly Arg Leu Ser Phe Thr Ser Gly Pro
                325                 330                 335

ccc acc ctg tct cta cag aaa aaa aaa att ttt ttt tca aaa ttc atg   1056
Pro Thr Leu Ser Leu Gln Lys Lys Lys Ile Phe Phe Ser Lys Phe Met
            340                 345                 350

gca gcc act aac cac gtg gct gtt caa cac tgg aaa tgt gcc ctg tcc   1104
Ala Ala Thr Asn His Val Ala Val Gln His Trp Lys Cys Ala Leu Ser
        355                 360                 365

aaa ctg aga cat gct ata aat gta aag cac acc aga ttt caa agc cat   1152
Lys Leu Arg His Ala Ile Asn Val Lys His Thr Arg Phe Gln Ser His
    370                 375                 380

gaa gat att ctg ggg gaa gtt ttg cca aat gcc ttc aat tta tat att   1200
Glu Asp Ile Leu Gly Glu Val Leu Pro Asn Ala Phe Asn Leu Tyr Ile
385                 390                 395                 400

caa tac att tct atc ata gca acc ttt ctg aaa aga gag ggt gag agg   1248
Gln Tyr Ile Ser Ile Ile Ala Thr Phe Leu Lys Arg Glu Gly Glu Arg
                405                 410                 415

aag aga gag aaa                                                  1260
Lys Arg Glu Lys
            420
```

<210> 26
<211> 420
<212> PRT
<213> Homo sapiens

<400> 26

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Glu Ser Ser Thr Leu Leu Glu Lys Tyr Lys Ile Gly Lys Val Ile Gly
 1               5                  10                  15
Asp Gly Asn Phe Ala Val Val Lys Glu Cys Ile Asp Arg Ser Thr Gly
            20                  25                  30
Lys Glu Phe Ala Leu Lys Ile Ile Asp Lys Ala Lys Cys Cys Gly Lys
        35                  40                  45
Glu His Leu Ile Glu Asn Glu Val Ser Ile Leu Arg Arg Val Lys His
    50                  55                  60
Pro Asn Ile Ile Met Leu Val Glu Glu Met Glu Thr Ala Thr Glu Leu
65                  70                  75                  80
```

```
Phe Leu Val Met Glu Leu Val Lys Gly Gly Asp Leu Phe Asp Ala Ile
                85                  90                  95
Thr Ser Ser Thr Lys Tyr Thr Glu Arg Asp Gly Ser Ala Met Val Tyr
            100                 105                 110
Asn Leu Ala Asn Ala Leu Arg Tyr Leu His Gly Leu Ser Ile Val His
        115                 120                 125
Arg Asp Ile Lys Pro Glu Asn Leu Leu Val Cys Glu Tyr Pro Asp Gly
    130                 135                 140
Thr Lys Ser Leu Lys Leu Gly Asp Phe Gly Leu Ala Thr Val Val Glu
145                 150                 155                 160
Gly Pro Leu Tyr Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu
                165                 170                 175
Ile Ile Ala Glu Thr Gly Tyr Gly Leu Lys Val Asp Ile Trp Ala Ala
            180                 185                 190
Gly Val Ile Thr Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser
        195                 200                 205
Glu Asn Asn Leu Gln Glu Asp Leu Phe Asp Gln Ile Leu Ala Gly Lys
    210                 215                 220
Leu Glu Phe Pro Ala Pro Tyr Trp Asp Asn Ile Thr Asp Ser Ala Lys
225                 230                 235                 240
Glu Leu Ile Ser Gln Met Leu Gln Val Asn Val Glu Ala Arg Cys Thr
                245                 250                 255
Ala Gly Gln Ile Leu Ser His Pro Trp Val Ser Pro Met Gln Pro Trp
            260                 265                 270
Ala Gly Arg Pro Ala His Arg Glu Gln Val Glu Ala Ser Gln Pro Pro
        275                 280                 285
Arg Gln Gly Pro Trp Phe Ser Pro His Thr Pro Arg Ser Arg Glu Gln
    290                 295                 300
Gly Trp Ser Gly Leu Ser Gln Ser Trp Ser Trp Leu Gln Gln Leu Ser
305                 310                 315                 320
Asn Gln Thr Cys Gln Gly Asp Gly Arg Leu Ser Phe Thr Ser Gly Pro
                325                 330                 335
Pro Thr Leu Ser Leu Gln Lys Lys Lys Ile Phe Phe Ser Lys Phe Met
            340                 345                 350
Ala Ala Thr Asn His Val Ala Val Gln His Trp Lys Cys Ala Leu Ser
        355                 360                 365
Lys Leu Arg His Ala Ile Asn Val Lys His Thr Arg Phe Gln Ser His
    370                 375                 380
Glu Asp Ile Leu Gly Glu Val Leu Pro Asn Ala Phe Asn Leu Tyr Ile
385                 390                 395                 400
Gln Tyr Ile Ser Ile Ile Ala Thr Phe Leu Lys Arg Glu Gly Glu Arg
                405                 410                 415
Lys Arg Glu Lys
            420
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<210> 27
<211> 1299
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1299)
<223> MOOSE03313

<400> 27

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gac gct gct gtc ctc aag cga cga ggc tac ctc ctg ggg ata aat tta   48
Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
 1               5                  10                  15
```

```
gga gag ggc tcc tat gca aaa gta aaa tct gct tac tct gag cgc ctg   96
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
            20                  25                  30

aag ttc aat gtg gcg atc aag atc atc gac cgc aag aag gcc ccc gca  144
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
        35                  40                  45

gac ttc ttg gag aaa ttc ctt ccc cgg gaa att gag att ctg gcc atg  192
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
    50                  55                  60

tta aac cac tgc tcc atc att aag acc tac gag atc ttt gag aca tca  240
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65                  70                  75                  80

cat ggc aag gtc tac atc gtc atg gag ctc gca gtc cag ggc gac ctc  288
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
                85                  90                  95

ctc gag tta atc aaa acc cgg gga gcc ctg cat gag gac gaa gct cgc  336
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
            100                 105                 110

aag aag ttc cac cag ctt tcc ttg gcc atc aag tac tgc cac gac ctg  384
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
        115                 120                 125

gac gtc gtc cac cgg gac ctc aag tgt gac aac ctt ctc ctt gac aag  432
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
    130                 135                 140

gac ttc aac atc aag ctg tcc gac ttc agc ttc tcc aag cgc tgc ctg  480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
145                 150                 155                 160

cgg gat gac agt ggt cga atg gcc tta agc aag acc ttc tgt ggg tca  528
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
                165                 170                 175

cca gcg tat gcg gcc cca gag gtg ctg cag ggc att ccc tac cag ccc  576
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
            180                 185                 190

aag gtg tac gac atc tgg agc cta ggc gtg atc ctc tac atc atg gtc  624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
        195                 200                 205

tgc ggc tcc atg ccc tac gac gac tcc aac atc aag aag atg ctg cgt  672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
    210                 215                 220

atc cag aag gag cac cgc gtc aac ttc cca cgc tcc aag cac ctg aca  720
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
225                 230                 235                 240

ggc gag tgc aag gac ctc atc tac cac atg ctg cag ccc gac gtc aac  768
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
                245                 250                 255
```

```
cgg cgg ctc cac atc gac gag atc ctc agc cac tgc tgg atg cag ccc   816
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
            260                 265                 270

aag gca cgg gga tct ccc tct gtg gcc atc aac aag gag ggg gag aat   864
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Asn
        275                 280                 285

aaa acc aca aag atg ggg aga aac cag agc aga aaa gct gaa aat tct   912
Lys Thr Thr Lys Met Gly Arg Asn Gln Ser Arg Lys Ala Glu Asn Ser
    290                 295                 300

aaa aac cag agt gcc ttt tct cct cca aag gat cac agc tcc tcg cca   960
Lys Asn Gln Ser Ala Phe Ser Pro Pro Lys Asp His Ser Ser Ser Pro
305                 310                 315                 320

gca atg gaa caa agc tgg acg gag aat gac ttt gac aag ctg aca gaa   1008
Ala Met Glu Gln Ser Trp Thr Glu Asn Asp Phe Asp Lys Leu Thr Glu
                325                 330                 335

gta ggc ttc aga agg tcg gta ata aca aac ttc tcc aag cta aag gag   1056
Val Gly Phe Arg Arg Ser Val Ile Thr Asn Phe Ser Lys Leu Lys Glu
            340                 345                 350

gat gtt cga acc cat cac aag gaa gct aaa agc ctt gaa aaa aga tta   1104
Asp Val Arg Thr His His Lys Glu Ala Lys Ser Leu Glu Lys Arg Leu
        355                 360                 365

gac caa tgg cta aat aga ata aac agt gta gag gag acc tta aat gac   1152
Asp Gln Trp Leu Asn Arg Ile Asn Ser Val Glu Glu Thr Leu Asn Asp
    370                 375                 380

ctg atg gag ctg aaa acc atg gca cga gaa cta cgt gac gca tgc aca   1200
Leu Met Glu Leu Lys Thr Met Ala Arg Glu Leu Arg Asp Ala Cys Thr
385                 390                 395                 400

aga ttt aat agc caa ttc gat caa gtg gaa gaa agg gta tca gtg att   1248
Arg Phe Asn Ser Gln Phe Asp Gln Val Glu Glu Arg Val Ser Val Ile
                405                 410                 415

gaa gat caa att aat gaa ata aag caa gaa gag aaa gtt aga gaa aaa   1296
Glu Asp Gln Ile Asn Glu Ile Lys Gln Glu Glu Lys Val Arg Glu Lys
            420                 425                 430

agc                                                               1299
Ser
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<210> 28
<211> 433
<212> PRT
<213> Homo sapiens

<400> 28

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Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
 1               5                  10                  15
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
            20                  25                  30
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
        35                  40                  45
```

```
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
    50                  55                  60
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65                  70                  75                  80
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
                85                  90                  95
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
            100                 105                 110
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
        115                 120                 125
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
    130                 135                 140
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
145                 150                 155                 160
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
                165                 170                 175
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
            180                 185                 190
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
        195                 200                 205
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
    210                 215                 220
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
225                 230                 235                 240
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
                245                 250                 255
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
            260                 265                 270
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Asn
        275                 280                 285
Lys Thr Thr Lys Met Gly Arg Asn Gln Ser Arg Lys Ala Glu Asn Ser
    290                 295                 300
Lys Asn Gln Ser Ala Phe Ser Pro Pro Lys Asp His Ser Ser Ser Pro
305                 310                 315                 320
Ala Met Glu Gln Ser Trp Thr Glu Asn Asp Phe Asp Lys Leu Thr Glu
                325                 330                 335
Val Gly Phe Arg Arg Ser Val Ile Thr Asn Phe Ser Lys Leu Lys Glu
            340                 345                 350
Asp Val Arg Thr His His Lys Glu Ala Lys Ser Leu Glu Lys Arg Leu
        355                 360                 365
Asp Gln Trp Leu Asn Arg Ile Asn Ser Val Glu Glu Thr Leu Asn Asp
    370                 375                 380
Leu Met Glu Leu Lys Thr Met Ala Arg Glu Leu Arg Asp Ala Cys Thr
385                 390                 395                 400
Arg Phe Asn Ser Gln Phe Asp Gln Val Glu Glu Arg Val Ser Val Ile
                405                 410                 415
Glu Asp Gln Ile Asn Glu Ile Lys Gln Glu Glu Lys Val Arg Glu Lys
            420                 425                 430
Ser
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<210> 29
<211> 1215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1215)
<223> MOOSE03314

<400> 29
gac gct gct gtc ctc aag cga cga ggc tac ctc ctg ggg ata aat tta 48
Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
1 5 10 15

gga gag ggc tcc tat gca aaa gta aaa tct gct tac tct gag cgc ctg 96
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
20 25 30

aag ttc aat gtg gcg atc aag atc atc gac cgc aag aag gcc ccc gca 144
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
35 40 45

gac ttc ttg gag aaa ttc ctt ccc cgg gaa att gag att ctg gcc atg 192
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
50 55 60

tta aac cac tgc tcc atc att aag acc tac gag atc ttt gag aca tca 240
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65 70 75 80

cat ggc aag gtc tac atc gtc atg gag ctc gcg gtc cag ggc gac ctc 288
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
85 90 95

ctc gag tta atc aaa acc cgg gga gcc ctg cat gag gac gaa gct cgc 336
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
100 105 110

aag aag ttc cac cag ctt tcc ttg gcc atc aag tac tgc cac gac ctg 384
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
115 120 125

gac gtc gtc cac cgg gac ctc aag tgt gac aac ctt ctc ctt gac aag 432
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
130 135 140

gac ttc aac atc aag ctg tcc gac ttc agc ttc tcc aag cgc tgc ctg 480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
145 150 155 160

cgg gat gac agt ggt cga atg gcc tta agc aag acc ttc tgt ggg tca 528
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
165 170 175

cca gcg tat gcg gcc cca gag gtg ctg cag ggc att ccc tac cag ccc 576
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
180 185 190

aag gtg tac gac atc tgg agc cta ggc gtg atc ctc tac atc atg gtc 624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
195 200 205

tgc ggc tcc atg ccc tac gac gac tcc aac atc aag aag atg ctg cgt 672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
210 215 220

atc cag aag gag cac cgc gtc aac ttc cca cgc tcc aag cac ctg aca 720
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
225 230 235 240

```
ggc gag tgc aag gac ctc atc tac cac atg ctg cag ccc gac gtc aac   768
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
                245                 250                 255

cgg cgg ctc cac atc gac gag atc ctc agc cac tgc tgg atg cag ccc   816
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
            260                 265                 270

aag gca cgg gga tct ccc tct gtg gcc atc aac aag gag ggg gag agt   864
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Ser
        275                 280                 285

tcc cgg gga act gaa ccc tta aca gaa gtc ata aca aac agt ctc tca   912
Ser Arg Gly Thr Glu Pro Leu Thr Glu Val Ile Thr Asn Ser Leu Ser
    290                 295                 300

gac cac agt gga atc aaa tta aaa ctc acg att aag aaa ctc act caa   960
Asp His Ser Gly Ile Lys Leu Lys Leu Thr Ile Lys Lys Leu Thr Gln
305                 310                 315                 320

aac tgc aca acc tca tgg aac ctg aac aac aac gtg ctc ctg aat gac   1008
Asn Cys Thr Thr Ser Trp Asn Leu Asn Asn Asn Val Leu Leu Asn Asp
                325                 330                 335

tac tgg gta aat aac gaa att aag gca gaa ata att aag ttc ttt gaa   1056
Tyr Trp Val Asn Asn Glu Ile Lys Ala Glu Ile Ile Lys Phe Phe Glu
            340                 345                 350

acc aat gag aac aaa gac aca tca tac cag aat ctc tgg aca cta gct   1104
Thr Asn Glu Asn Lys Asp Thr Ser Tyr Gln Asn Leu Trp Thr Leu Ala
        355                 360                 365

aaa gca gtg ttt aga ggg aaa ttt ata gaa cta aat gcc cac aag aga   1152
Lys Ala Val Phe Arg Gly Lys Phe Ile Glu Leu Asn Ala His Lys Arg
    370                 375                 380

aag cag gaa agg tct aaa att gac acc cta aca tca caa tta aag gaa   1200
Lys Gln Glu Arg Ser Lys Ile Asp Thr Leu Thr Ser Gln Leu Lys Glu
385                 390                 395                 400

cta gaa agc aga gca                                              1215
Leu Glu Ser Arg Ala
                405
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<210> 30
<211> 405
<212> PRT
<213> Homo sapiens

<400> 30

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Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
 1               5                  10                  15
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
            20                  25                  30
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
        35                  40                  45
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
    50                  55                  60
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65                  70                  75                  80
```

```
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
                85                  90                  95
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
            100                 105                 110
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
        115                 120                 125
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
    130                 135                 140
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
145                 150                 155                 160
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
                165                 170                 175
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
            180                 185                 190
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
        195                 200                 205
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
    210                 215                 220
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
225                 230                 235                 240
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
                245                 250                 255
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
            260                 265                 270
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Ser
        275                 280                 285
Ser Arg Gly Thr Glu Pro Leu Thr Glu Val Ile Thr Asn Ser Leu Ser
    290                 295                 300
Asp His Ser Gly Ile Lys Leu Lys Leu Thr Ile Lys Lys Leu Thr Gln
305                 310                 315                 320
Asn Cys Thr Thr Ser Trp Asn Leu Asn Asn Asn Val Leu Leu Asn Asp
                325                 330                 335
Tyr Trp Val Asn Asn Glu Ile Lys Ala Glu Ile Ile Lys Phe Phe Glu
            340                 345                 350
Thr Asn Glu Asn Lys Asp Thr Ser Tyr Gln Asn Leu Trp Thr Leu Ala
        355                 360                 365
Lys Ala Val Phe Arg Gly Lys Phe Ile Glu Leu Asn Ala His Lys Arg
    370                 375                 380
Lys Gln Glu Arg Ser Lys Ile Asp Thr Leu Thr Ser Gln Leu Lys Glu
385                 390                 395                 400
Leu Glu Ser Arg Ala
                405
```

<210> 31
<211> 1095
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1095)
<223> MOOSE03316

<400> 31

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gat gcc aca gtc cta agg aag aag ggt tac atc gta ggc atc aat ctt   48
Asp Ala Thr Val Leu Arg Lys Lys Gly Tyr Ile Val Gly Ile Asn Leu
 1               5                  10                  15

ggc aag ggt tcc tac gca aaa gtc aaa tct gcc tac tct gag cgc ctc   96
Gly Lys Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
            20                  25                  30
```

```
aag ttc aat gtg gct gtc aag atc atc gac cgc aag aaa aca cct act   144
Lys Phe Asn Val Ala Val Lys Ile Ile Asp Arg Lys Lys Thr Pro Thr
         35                  40                  45

gac ttt gtg gag aga ttc ctt cct cgg gag atg gac atc ctg gca act   192
Asp Phe Val Glu Arg Phe Leu Pro Arg Glu Met Asp Ile Leu Ala Thr
     50                  55                  60

gtc aac cac ggc tcc atc atc aag act tac gag atc ttt gag acc tct   240
Val Asn His Gly Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
 65                  70                  75                  80

gac gga cgg atc tac atc atc atg gag ctt ggc gtc cag ggc gac ctc   288
Asp Gly Arg Ile Tyr Ile Ile Met Glu Leu Gly Val Gln Gly Asp Leu
                 85                  90                  95

ctc gag ttc atc aag tgc cag gga gcc ctg cat gag gac gtg gca cgc   336
Leu Glu Phe Ile Lys Cys Gln Gly Ala Leu His Glu Asp Val Ala Arg
            100                 105                 110

aag atg ttc cga cag ctc tcc tcc gcc gtc aag tac tgc cac gac ctg   384
Lys Met Phe Arg Gln Leu Ser Ser Ala Val Lys Tyr Cys His Asp Leu
        115                 120                 125

gac atc gtc cac cgg gac ctc aag tgc gag aac ctt ctc ctc gac aag   432
Asp Ile Val His Arg Asp Leu Lys Cys Glu Asn Leu Leu Leu Asp Lys
    130                 135                 140

gac ttc aac atc aag ctg tct gac ttt ggc ttc tcc aag cgc tgc ctg   480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Gly Phe Ser Lys Arg Cys Leu
145                 150                 155                 160

cgg gac agc aat ggg cgc atc atc ctc agc aag acc ttc tgc ggg tcg   528
Arg Asp Ser Asn Gly Arg Ile Ile Leu Ser Lys Thr Phe Cys Gly Ser
                165                 170                 175

gca gca tat gca gcc ccc gag gtg ctg cag agc atc ccc tac cag ccc   576
Ala Ala Tyr Ala Ala Pro Glu Val Leu Gln Ser Ile Pro Tyr Gln Pro
            180                 185                 190

aag gtg tat gac atc tgg agc ctg ggc gtg atc ctg tac atc atg gtc   624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
        195                 200                 205

tgc ggc tcc atg ccc tat gac gac tcc gac atc agg aag atg ctg cgt   672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asp Ile Arg Lys Met Leu Arg
    210                 215                 220

atc cag aag gag cac cgt gtg gac ttc ccg cgc tcc aag aac ctg acc   720
Ile Gln Lys Glu His Arg Val Asp Phe Pro Arg Ser Lys Asn Leu Thr
225                 230                 235                 240

tgc gag tgc aag gac ctc atc tac cgc atg ctg cag ccc gac gtc agc   768
Cys Glu Cys Lys Asp Leu Ile Tyr Arg Met Leu Gln Pro Asp Val Ser
                245                 250                 255

cag cgg ctc cac atc gat gag atc ctc agc cac tcg tgg ctg cag ccc   816
Gln Arg Leu His Ile Asp Glu Ile Leu Ser His Ser Trp Leu Gln Pro
            260                 265                 270
```

```
ccc aag ccc aaa gcc acg tct tct gcc tcc ttc aag agg gag ggg gag   864
Pro Lys Pro Lys Ala Thr Ser Ser Ala Ser Phe Lys Arg Glu Gly Glu
        275                 280                 285

ggc aag tac cgc gct gag tgc aaa ctg gac acc aag aca ggc ttg agg   912
Gly Lys Tyr Arg Ala Glu Cys Lys Leu Asp Thr Lys Thr Gly Leu Arg
    290                 295                 300

ccc gac cac cgg ccc gac cac aag ctt gga gcc aaa acc cag cac cgg   960
Pro Asp His Arg Pro Asp His Lys Leu Gly Ala Lys Thr Gln His Arg
305                 310                 315                 320

ctg ctg gtg ggg aac cta agg gta caa ctt cca agg gct ccg ttt ctc   1008
Leu Leu Val Gly Asn Leu Arg Val Gln Leu Pro Arg Ala Pro Phe Leu
                325                 330                 335

ctt cat atc ccc cca gag aag cag aaa gca ctg cag gat gtg agc tca   1056
Leu His Ile Pro Pro Glu Lys Gln Lys Ala Leu Gln Asp Val Ser Ser
            340                 345                 350

act cag aac aca ggt tcc gag tgc cgc aga aag caa cgc               1095
Thr Gln Asn Thr Gly Ser Glu Cys Arg Arg Lys Gln Arg
        355                 360                 365
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<210> 32
<211> 365
<212> PRT
<213> Homo sapiens

<400> 32

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Asp Ala Thr Val Leu Arg Lys Lys Gly Tyr Ile Val Gly Ile Asn Leu
 1               5                  10                  15
Gly Lys Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
            20                  25                  30
Lys Phe Asn Val Ala Val Lys Ile Ile Asp Arg Lys Lys Thr Pro Thr
        35                  40                  45
Asp Phe Val Glu Arg Phe Leu Pro Arg Glu Met Asp Ile Leu Ala Thr
    50                  55                  60
Val Asn His Gly Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65                  70                  75                  80
Asp Gly Arg Ile Tyr Ile Ile Met Glu Leu Gly Val Gln Gly Asp Leu
                85                  90                  95
Leu Glu Phe Ile Lys Cys Gln Gly Ala Leu His Glu Asp Val Ala Arg
            100                 105                 110
Lys Met Phe Arg Gln Leu Ser Ser Ala Val Lys Tyr Cys His Asp Leu
        115                 120                 125
Asp Ile Val His Arg Asp Leu Lys Cys Glu Asn Leu Leu Leu Asp Lys
    130                 135                 140
Asp Phe Asn Ile Lys Leu Ser Asp Phe Gly Phe Ser Lys Arg Cys Leu
145                 150                 155                 160
Arg Asp Ser Asn Gly Arg Ile Ile Leu Ser Lys Thr Phe Cys Gly Ser
                165                 170                 175
Ala Ala Tyr Ala Ala Pro Glu Val Leu Gln Ser Ile Pro Tyr Gln Pro
            180                 185                 190
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
        195                 200                 205
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asp Ile Arg Lys Met Leu Arg
    210                 215                 220
Ile Gln Lys Glu His Arg Val Asp Phe Pro Arg Ser Lys Asn Leu Thr
225                 230                 235                 240
```

```
Cys Glu Cys Lys Asp Leu Ile Tyr Arg Met Leu Gln Pro Asp Val Ser
                245                 250                 255
Gln Arg Leu His Ile Asp Glu Ile Leu Ser His Ser Trp Leu Gln Pro
            260                 265                 270
Pro Lys Pro Lys Ala Thr Ser Ser Ala Ser Phe Lys Arg Glu Gly Glu
        275                 280                 285
Gly Lys Tyr Arg Ala Glu Cys Lys Leu Asp Thr Lys Thr Gly Leu Arg
    290                 295                 300
Pro Asp His Arg Pro Asp His Lys Leu Gly Ala Lys Thr Gln His Arg
305                 310                 315                 320
Leu Leu Val Gly Asn Leu Arg Val Gln Leu Pro Arg Ala Pro Phe Leu
                325                 330                 335
Leu His Ile Pro Pro Glu Lys Gln Lys Ala Leu Gln Asp Val Ser Ser
            340                 345                 350
Thr Gln Asn Thr Gly Ser Glu Cys Arg Arg Lys Gln Arg
        355                 360                 365


<210> 33
<211> 1260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1260)
<223> MOOSE03330

<400> 33
agc atg gag gac ttt ctg ctc tcc aat ggg tac cag ctg ggc aag acc   48
Ser Met Glu Asp Phe Leu Leu Ser Asn Gly Tyr Gln Leu Gly Lys Thr
 1               5                  10                  15

att ggg gaa ggg acc tac tca aaa gtc aaa gaa gca ttt tcc aaa aaa   96
Ile Gly Glu Gly Thr Tyr Ser Lys Val Lys Glu Ala Phe Ser Lys Lys
             20                  25                  30

cac caa aga aaa gtg gca att aaa gtt ata gac aag atg gga ggg cca   144
His Gln Arg Lys Val Ala Ile Lys Val Ile Asp Lys Met Gly Gly Pro
         35                  40                  45

gaa gag ttt atc cag aga ttc ctc cct cgg gag ctc caa atc gtc cgt   192
Glu Glu Phe Ile Gln Arg Phe Leu Pro Arg Glu Leu Gln Ile Val Arg
     50                  55                  60

acc ctg gac cac aag aac atc atc cag gtg tat gag atg ctg gag tct   240
Thr Leu Asp His Lys Asn Ile Ile Gln Val Tyr Glu Met Leu Glu Ser
 65                  70                  75                  80

gcc gac ggg aaa atc tgc ctg gtg atg gag ctc gct gag gga ggg gat   288
Ala Asp Gly Lys Ile Cys Leu Val Met Glu Leu Ala Glu Gly Gly Asp
                 85                  90                  95

gtc ttt gac tgc gtg ctg aat ggg ggg cca ctg cct gaa agc cgg gcc   336
Val Phe Asp Cys Val Leu Asn Gly Gly Pro Leu Pro Glu Ser Arg Ala
            100                 105                 110

aag gcc ctc ttc cgt cag atg gtt gag gcc atc cgc tac tgc cat ggc   384
Lys Ala Leu Phe Arg Gln Met Val Glu Ala Ile Arg Tyr Cys His Gly
        115                 120                 125
```

```
tgt ggt gtg gcc cac cgg gac ctc aaa tgt gag aac gcc ttg ttg cag   432
Cys Gly Val Ala His Arg Asp Leu Lys Cys Glu Asn Ala Leu Leu Gln
    130                 135                 140

ggc ttc aac ctg aag ctg act gac ttt ggc ttt gcc aag gtg ttg ccc   480
Gly Phe Asn Leu Lys Leu Thr Asp Phe Gly Phe Ala Lys Val Leu Pro
145                 150                 155                 160

aag tca cac cgg gag ctg agc cag acc ttc tgc ggc agt aca gcc tat   528
Lys Ser His Arg Glu Leu Ser Gln Thr Phe Cys Gly Ser Thr Ala Tyr
                165                 170                 175

gct gcc ccc gag gtg ctg cag ggc att ccc cac gat agc aaa aaa ggt   576
Ala Ala Pro Glu Val Leu Gln Gly Ile Pro His Asp Ser Lys Lys Gly
            180                 185                 190

gat gtc tgg agc atg ggt gtg gtc ctg tat gtc atg ctc tgt gcc agc   624
Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Leu Cys Ala Ser
        195                 200                 205

cta cct ttt gac gac aca gac atc ccc aag atg ctg tgg cag cag cag   672
Leu Pro Phe Asp Asp Thr Asp Ile Pro Lys Met Leu Trp Gln Gln Gln
    210                 215                 220

aag ggg gtg tcc ttc ccc act cat ctg agc atc tcg gcc gat tgc cag   720
Lys Gly Val Ser Phe Pro Thr His Leu Ser Ile Ser Ala Asp Cys Gln
225                 230                 235                 240

gac ctg ctc aag agg ctc ctg gaa ccc gat atg atc ctc cgg cct tca   768
Asp Leu Leu Lys Arg Leu Leu Glu Pro Asp Met Ile Leu Arg Pro Ser
                245                 250                 255

att gaa gaa gtt aag cag cat cgc tgg ttt caa act cct gac ctc aat   816
Ile Glu Glu Val Lys Gln His Arg Trp Phe Gln Thr Pro Asp Leu Asn
            260                 265                 270

gat ctg gcc acc tcg gcc tcc caa gat act ggg cat aga aag cac cct   864
Asp Leu Ala Thr Ser Ala Ser Gln Asp Thr Gly His Arg Lys His Pro
        275                 280                 285

ttc tct gcc agg ata ctc agt caa cca caa tcc agc ttc tcc ctt gaa   912
Phe Ser Ala Arg Ile Leu Ser Gln Pro Gln Ser Ser Phe Ser Leu Glu
    290                 295                 300

att cag aat gct gag ctg gct tct cct gct cac tgg ggg aaa gtt cag   960
Ile Gln Asn Ala Glu Leu Ala Ser Pro Ala His Trp Gly Lys Val Gln
305                 310                 315                 320

cct cca cag gag gac ctg gag gct cag ctg ggg tcc ctt ggt ggg ttg  1008
Pro Pro Gln Glu Asp Leu Glu Ala Gln Leu Gly Ser Leu Gly Gly Leu
                325                 330                 335

cag aag gtt tcg tct cct cag ggt gct ctg gtg tct gag ctg gca atg  1056
Gln Lys Val Ser Ser Pro Gln Gly Ala Leu Val Ser Glu Leu Ala Met
            340                 345                 350

gag atg caa tcc tat tat gcc aag ctt ttg ggg gag ctg aat gaa cag  1104
Glu Met Gln Ser Tyr Tyr Ala Lys Leu Leu Gly Glu Leu Asn Glu Gln
        355                 360                 365
```

```
aga aag agg gac ttt ttc tgt gac tgc agc atc att gtg gaa ggg cgg   1152
Arg Lys Arg Asp Phe Phe Cys Asp Cys Ser Ile Ile Val Glu Gly Arg
    370                 375                 380

atc ttc aag gcc cac agg aac att ttg ttt gct aac agc ggc tac ttc   1200
Ile Phe Lys Ala His Arg Asn Ile Leu Phe Ala Asn Ser Gly Tyr Phe
385                 390                 395                 400

cga gcc ctg ctc att cac tat atc cag gac agc ggg cgg cat agc acc   1248
Arg Ala Leu Leu Ile His Tyr Ile Gln Asp Ser Gly Arg His Ser Thr
                405                 410                 415

gcc tcc ttg gac                                                  1260
Ala Ser Leu Asp
            420
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<210> 34
<211> 420
<212> PRT
<213> Homo sapiens

<400> 34

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Ser Met Glu Asp Phe Leu Leu Ser Asn Gly Tyr Gln Leu Gly Lys Thr
 1               5                  10                  15
Ile Gly Glu Gly Thr Tyr Ser Lys Val Lys Glu Ala Phe Ser Lys Lys
            20                  25                  30
His Gln Arg Lys Val Ala Ile Lys Val Ile Asp Lys Met Gly Gly Pro
        35                  40                  45
Glu Glu Phe Ile Gln Arg Phe Leu Pro Arg Glu Leu Gln Ile Val Arg
    50                  55                  60
Thr Leu Asp His Lys Asn Ile Ile Gln Val Tyr Glu Met Leu Glu Ser
65                  70                  75                  80
Ala Asp Gly Lys Ile Cys Leu Val Met Glu Leu Ala Glu Gly Gly Asp
                85                  90                  95
Val Phe Asp Cys Val Leu Asn Gly Gly Pro Leu Pro Glu Ser Arg Ala
            100                 105                 110
Lys Ala Leu Phe Arg Gln Met Val Glu Ala Ile Arg Tyr Cys His Gly
        115                 120                 125
Cys Gly Val Ala His Arg Asp Leu Lys Cys Glu Asn Ala Leu Leu Gln
    130                 135                 140
Gly Phe Asn Leu Lys Leu Thr Asp Phe Gly Phe Ala Lys Val Leu Pro
145                 150                 155                 160
Lys Ser His Arg Glu Leu Ser Gln Thr Phe Cys Gly Ser Thr Ala Tyr
                165                 170                 175
Ala Ala Pro Glu Val Leu Gln Gly Ile Pro His Asp Ser Lys Lys Gly
            180                 185                 190
Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Leu Cys Ala Ser
        195                 200                 205
Leu Pro Phe Asp Asp Thr Asp Ile Pro Lys Met Leu Trp Gln Gln Gln
    210                 215                 220
Lys Gly Val Ser Phe Pro Thr His Leu Ser Ile Ser Ala Asp Cys Gln
225                 230                 235                 240
Asp Leu Leu Lys Arg Leu Leu Glu Pro Asp Met Ile Leu Arg Pro Ser
                245                 250                 255
Ile Glu Glu Val Lys Gln His Arg Trp Phe Gln Thr Pro Asp Leu Asn
            260                 265                 270
Asp Leu Ala Thr Ser Ala Ser Gln Asp Thr Gly His Arg Lys His Pro
        275                 280                 285
Phe Ser Ala Arg Ile Leu Ser Gln Pro Gln Ser Ser Phe Ser Leu Glu
    290                 295                 300
```

```
Ile Gln Asn Ala Glu Leu Ala Ser Pro Ala His Trp Gly Lys Val Gln
305                 310                 315                 320
Pro Pro Gln Glu Asp Leu Glu Ala Gln Leu Gly Ser Leu Gly Gly Leu
                325                 330                 335
Gln Lys Val Ser Ser Pro Gln Gly Ala Leu Val Ser Glu Leu Ala Met
            340                 345                 350
Glu Met Gln Ser Tyr Tyr Ala Lys Leu Leu Gly Glu Leu Asn Glu Gln
        355                 360                 365
Arg Lys Arg Asp Phe Phe Cys Asp Cys Ser Ile Ile Val Glu Gly Arg
    370                 375                 380
Ile Phe Lys Ala His Arg Asn Ile Leu Phe Ala Asn Ser Gly Tyr Phe
385                 390                 395                 400
Arg Ala Leu Leu Ile His Tyr Ile Gln Asp Ser Gly Arg His Ser Thr
                405                 410                 415
Ala Ser Leu Asp
            420
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<210> 35
<211> 1128
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1128)
<223> MOOSE03332

<400> 35

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aag ctt tac aaa tta gag aga tcg tac att agc aag cta acc cta ggg   48
Lys Leu Tyr Lys Leu Glu Arg Ser Tyr Ile Ser Lys Leu Thr Leu Gly
 1               5                  10                  15

caa tta cat ttt gga aaa ggg cgt ttc ggc cag gtt cac aag tgt gag   96
Gln Leu His Phe Gly Lys Gly Arg Phe Gly Gln Val His Lys Cys Glu
            20                  25                  30

gag acg gcc aca ggt ctg aag ctg gca gcc aaa atc atc aag acc aga   144
Glu Thr Ala Thr Gly Leu Lys Leu Ala Ala Lys Ile Ile Lys Thr Arg
        35                  40                  45

ggc atg aag gac aag gta cag cct gag gag gtg aag aac gag atc agc   192
Gly Met Lys Asp Lys Val Gln Pro Glu Glu Val Lys Asn Glu Ile Ser
    50                  55                  60

gtc atg aac cag ctg gac cac gcg aac ctc atc cag ctg tac gat gcc   240
Val Met Asn Gln Leu Asp His Ala Asn Leu Ile Gln Leu Tyr Asp Ala
65                  70                  75                  80

ttc gag tct aag aac gac att gtc ctg gtc atg gag tat gtg gat ggt   288
Phe Glu Ser Lys Asn Asp Ile Val Leu Val Met Glu Tyr Val Asp Gly
                85                  90                  95

ggg gag ctg ttt gac cgc atc atc gat gag agc tac aat ttg acg gag   336
Gly Glu Leu Phe Asp Arg Ile Ile Asp Glu Ser Tyr Asn Leu Thr Glu
            100                 105                 110

ctt gat acc atc ctg ttc atg aag cag ata tgt gag ggg ata agg cac   384
Leu Asp Thr Ile Leu Phe Met Lys Gln Ile Cys Glu Gly Ile Arg His
        115                 120                 125
```

```
atg cat cag atg tac att ctc cac ttg gac ctg aag cct gag aat atc   432
Met His Gln Met Tyr Ile Leu His Leu Asp Leu Lys Pro Glu Asn Ile
    130                 135                 140

ctg tgt gtg aat cgg gat gct aag caa ata aaa att att gat ttt gga   480
Leu Cys Val Asn Arg Asp Ala Lys Gln Ile Lys Ile Ile Asp Phe Gly
145                 150                 155                 160

ttg gcc aga agg tat aag ctg aag gtg aac ttt gga acc cca gaa ttt   528
Leu Ala Arg Arg Tyr Lys Leu Lys Val Asn Phe Gly Thr Pro Glu Phe
                165                 170                 175

ctc gcc cct gaa gtt gtg aac tat gat ttt gtt tca ttt ccc act gac   576
Leu Ala Pro Glu Val Val Asn Tyr Asp Phe Val Ser Phe Pro Thr Asp
            180                 185                 190

atg tgg agt gtg ggg gtc atc gcc tat atg cta ctt agc ggt ttg tcg   624
Met Trp Ser Val Gly Val Ile Ala Tyr Met Leu Leu Ser Gly Leu Ser
        195                 200                 205

cct ttc ctg ggt gac aat gat gct gag acg ctg aac aac atc ctg gcc   672
Pro Phe Leu Gly Asp Asn Asp Ala Glu Thr Leu Asn Asn Ile Leu Ala
    210                 215                 220

tgc agg tgg gac tta gag gat gaa gaa ttt cag gac atc tcg gag gag   720
Cys Arg Trp Asp Leu Glu Asp Glu Glu Phe Gln Asp Ile Ser Glu Glu
225                 230                 235                 240

gcc aag gag ttc atc tct aag ctt ctg att aag gag aag agt tgg cga   768
Ala Lys Glu Phe Ile Ser Lys Leu Leu Ile Lys Glu Lys Ser Trp Arg
                245                 250                 255

ata agt gca agc gaa gct ctc aag cac ccc tgg ttg tca gac cac aag   816
Ile Ser Ala Ser Glu Ala Leu Lys His Pro Trp Leu Ser Asp His Lys
            260                 265                 270

ctc cac tcc aga ctc aat gcc cag gtg acc acg gct tct tgc tct tcc   864
Leu His Ser Arg Leu Asn Ala Gln Val Thr Thr Ala Ser Cys Ser Ser
        275                 280                 285

tct ttt tct cct cgg ggc ctg cgg gcg cgg cgt ggc ggg gcg gga aaa   912
Ser Phe Ser Pro Arg Gly Leu Arg Ala Arg Arg Gly Gly Ala Gly Lys
    290                 295                 300

cgg ctc tgt ccc gtg ggg cgc agg cag gaa cgg att gcc cag gaa ggt   960
Arg Leu Cys Pro Val Gly Arg Arg Gln Glu Arg Ile Ala Gln Glu Gly
305                 310                 315                 320

atg gag gac cga aaa tgg atc acc agc cct cat gga caa ctt aaa cta  1008
Met Glu Asp Arg Lys Trp Ile Thr Ser Pro His Gly Gln Leu Lys Leu
                325                 330                 335

aag gtg gaa aag aca gaa aag ctg gca ggg gga att gtc tcc agc caa  1056
Lys Val Glu Lys Thr Glu Lys Leu Ala Gly Gly Ile Val Ser Ser Gln
            340                 345                 350

cct gtc aac ttt tgg aaa aag atg gat cac aaa gaa tgg gaa gtg gaa  1104
Pro Val Asn Phe Trp Lys Lys Met Asp His Lys Glu Trp Glu Val Glu
        355                 360                 365
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gag aag gag agg aga aac caa gaa 1128
Glu Lys Glu Arg Arg Asn Gln Glu
370 375

<210> 36
<211> 376
<212> PRT
<213> Homo sapiens

<400> 36
Lys Leu Tyr Lys Leu Glu Arg Ser Tyr Ile Ser Lys Leu Thr Leu Gly
1 5 10 15
Gln Leu His Phe Gly Lys Gly Arg Phe Gly Gln Val His Lys Cys Glu
20 25 30
Glu Thr Ala Thr Gly Leu Lys Leu Ala Ala Lys Ile Ile Lys Thr Arg
35 40 45
Gly Met Lys Asp Lys Val Gln Pro Glu Glu Val Lys Asn Glu Ile Ser
50 55 60
Val Met Asn Gln Leu Asp His Ala Asn Leu Ile Gln Leu Tyr Asp Ala
65 70 75 80
Phe Glu Ser Lys Asn Asp Ile Val Leu Val Met Glu Tyr Val Asp Gly
85 90 95
Gly Glu Leu Phe Asp Arg Ile Ile Asp Glu Ser Tyr Asn Leu Thr Glu
100 105 110
Leu Asp Thr Ile Leu Phe Met Lys Gln Ile Cys Glu Gly Ile Arg His
115 120 125
Met His Gln Met Tyr Ile Leu His Leu Asp Leu Lys Pro Glu Asn Ile
130 135 140
Leu Cys Val Asn Arg Asp Ala Lys Gln Ile Lys Ile Ile Asp Phe Gly
145 150 155 160
Leu Ala Arg Arg Tyr Lys Leu Lys Val Asn Phe Gly Thr Pro Glu Phe
165 170 175
Leu Ala Pro Glu Val Val Asn Tyr Asp Phe Val Ser Phe Pro Thr Asp
180 185 190
Met Trp Ser Val Gly Val Ile Ala Tyr Met Leu Leu Ser Gly Leu Ser
195 200 205
Pro Phe Leu Gly Asp Asn Asp Ala Glu Thr Leu Asn Asn Ile Leu Ala
210 215 220
Cys Arg Trp Asp Leu Glu Asp Glu Glu Phe Gln Asp Ile Ser Glu Glu
225 230 235 240
Ala Lys Glu Phe Ile Ser Lys Leu Leu Ile Lys Glu Lys Ser Trp Arg
245 250 255
Ile Ser Ala Ser Glu Ala Leu Lys His Pro Trp Leu Ser Asp His Lys
260 265 270
Leu His Ser Arg Leu Asn Ala Gln Val Thr Thr Ala Ser Cys Ser Ser
275 280 285
Ser Phe Ser Pro Arg Gly Leu Arg Ala Arg Arg Gly Gly Ala Gly Lys
290 295 300
Arg Leu Cys Pro Val Gly Arg Arg Gln Glu Arg Ile Ala Gln Glu Gly
305 310 315 320
Met Glu Asp Arg Lys Trp Ile Thr Ser Pro His Gly Gln Leu Lys Leu
325 330 335
Lys Val Glu Lys Thr Glu Lys Leu Ala Gly Gly Ile Val Ser Ser Gln
340 345 350
Pro Val Asn Phe Trp Lys Lys Met Asp His Lys Glu Trp Glu Val Glu
355 360 365
Glu Lys Glu Arg Arg Asn Gln Glu
370 375

<210> 37

<211> 1230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1230)
<223> MOOSE03340

<400> 37

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aaa aca aag caa aac aaa aca aaa caa aga ctc tac ctg ggg ctt ggc   48
Lys Thr Lys Gln Asn Lys Thr Lys Gln Arg Leu Tyr Leu Gly Leu Gly
 1               5                  10                  15

aag ttt ggg gca gtc tgt acc tgc atg gag aaa gcc aca ggc ctc aag   96
Lys Phe Gly Ala Val Cys Thr Cys Met Glu Lys Ala Thr Gly Leu Lys
            20                  25                  30

ctg gca gcc aag gtc atc aag aaa cag act ccc aaa gac aag gta gaa   144
Leu Ala Ala Lys Val Ile Lys Lys Gln Thr Pro Lys Asp Lys Val Glu
        35                  40                  45

atg gtg ttg ctg gag att gag gtc atg aac cag ctg aac cac cgc aat   192
Met Val Leu Leu Glu Ile Glu Val Met Asn Gln Leu Asn His Arg Asn
    50                  55                  60

ctg atc cag ctg tat gca gcc atc gag act ccg cat gag atc gtc ctg   240
Leu Ile Gln Leu Tyr Ala Ala Ile Glu Thr Pro His Glu Ile Val Leu
65                  70                  75                  80

ttc atg gag tac atc gag ggc gga gag ctc ttc gag agg att gtg gat   288
Phe Met Glu Tyr Ile Glu Gly Gly Glu Leu Phe Glu Arg Ile Val Asp
                85                  90                  95

gag gac tac cat ctg acc gag gtg gac acc atg gtg ttt gtc agg cag   336
Glu Asp Tyr His Leu Thr Glu Val Asp Thr Met Val Phe Val Arg Gln
            100                 105                 110

atc tgt gac ggg atc ctc ttc atg cac aag atg agg gtt ttg cac ctg   384
Ile Cys Asp Gly Ile Leu Phe Met His Lys Met Arg Val Leu His Leu
        115                 120                 125

gac ctc aag cca gag aac atc ctg tgt gtc aac acc acc ggg cat ttg   432
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu
    130                 135                 140

gtg aag atc att gac ttt ggc ctg gca cgg agg tac cac ctg ggt ggg   480
Val Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr His Leu Gly Gly
145                 150                 155                 160

tgg gga ggg caa gac aag cct ctg agt tgg cag ggg aca ggg gtg ggg   528
Trp Gly Gly Gln Asp Lys Pro Leu Ser Trp Gln Gly Thr Gly Val Gly
                165                 170                 175

tgg agg ggg cat ggg tat agg cca gga gct gtg ctc tca gcc ctt ggt   576
Trp Arg Gly His Gly Tyr Arg Pro Gly Ala Val Leu Ser Ala Leu Gly
            180                 185                 190

ctc acc ccc agg tat aac ccc aac gag aag ctg aag gtg aac ttt ggg   624
Leu Thr Pro Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val Asn Phe Gly
        195                 200                 205
```

```
acc cca gag ttc ctg tca cct gag gtg gtg aat tat gac caa atc tcc   672
Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp Gln Ile Ser
    210                 215                 220

gat aag aca gac atg tgg agt atg ggg gtg atc acc tac atg ctg ctg   720
Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr Met Leu Leu
225                 230                 235                 240

agc ggc ctc tcc ccc ttc ctg gga gat gat gac aca gag acc cta aac   768
Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu Thr Leu Asn
                245                 250                 255

aac gtt cta tct ggc aac tgg tac ttt gat gaa gag acc ttt gag gcc   816
Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr Phe Glu Ala
            260                 265                 270

gta tca gac gag gcc aaa gac ttt gtc tcc aac ctc atc gtc aag gac   864
Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile Val Lys Asp
        275                 280                 285

cag agg gcc cgg atg aac gct gcc cag tgt ctc gcc cat ccc tgg ctc   912
Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His Pro Trp Leu
    290                 295                 300

aac aac ctg gcg gag aaa gcc aaa cgc tgt aac cga cgc ctt aag tcc   960
Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg Leu Lys Ser
305                 310                 315                 320

cag atc ttg ctt aag aaa tac ctc atg aag agg cgc tgg aag gta ccg  1008
Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp Lys Val Pro
                325                 330                 335

ctg gat tca gga aag aaa gaa aga gag aga gag aaa gaa aga aag aaa  1056
Leu Asp Ser Gly Lys Lys Glu Arg Glu Arg Glu Lys Glu Arg Lys Lys
            340                 345                 350

gaa aga aag aaa gaa aga aag aaa gaa aga aag aaa aag gaa gga agg  1104
Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Lys Glu Gly Arg
        355                 360                 365

aag aaa gaa aga aag aaa gag aaa gaa aga aag aaa aag aaa gaa agg  1152
Lys Lys Glu Arg Lys Lys Glu Lys Glu Arg Lys Lys Lys Lys Glu Arg
    370                 375                 380

aag gaa gga agg aag gaa gga agg aag aaa gaa aga aag aaa gaa aga  1200
Lys Glu Gly Arg Lys Glu Gly Arg Lys Lys Glu Arg Lys Lys Glu Arg
385                 390                 395                 400

aag aaa gaa aga aag aaa gaa aga aag aaa                         1230
Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys
                405                 410
```

<210> 38
<211> 410
<212> PRT
<213> Homo sapiens

<400> 38

```
Lys Thr Lys Gln Asn Lys Thr Lys Gln Arg Leu Tyr Leu Gly Leu Gly
 1               5                  10                  15
```

```
Lys Phe Gly Ala Val Cys Thr Cys Met Glu Lys Ala Thr Gly Leu Lys
            20                  25                  30
Leu Ala Ala Lys Val Ile Lys Lys Gln Thr Pro Lys Asp Lys Val Glu
        35                  40                  45
Met Val Leu Leu Glu Ile Glu Val Met Asn Gln Leu Asn His Arg Asn
    50                  55                  60
Leu Ile Gln Leu Tyr Ala Ala Ile Glu Thr Pro His Glu Ile Val Leu
65                  70                  75                  80
Phe Met Glu Tyr Ile Glu Gly Gly Glu Leu Phe Glu Arg Ile Val Asp
                85                  90                  95
Glu Asp Tyr His Leu Thr Glu Val Asp Thr Met Val Phe Val Arg Gln
            100                 105                 110
Ile Cys Asp Gly Ile Leu Phe Met His Lys Met Arg Val Leu His Leu
        115                 120                 125
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu
    130                 135                 140
Val Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr His Leu Gly Gly
145                 150                 155                 160
Trp Gly Gly Gln Asp Lys Pro Leu Ser Trp Gln Gly Thr Gly Val Gly
                165                 170                 175
Trp Arg Gly His Gly Tyr Arg Pro Gly Ala Val Leu Ser Ala Leu Gly
            180                 185                 190
Leu Thr Pro Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val Asn Phe Gly
        195                 200                 205
Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp Gln Ile Ser
    210                 215                 220
Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr Met Leu Leu
225                 230                 235                 240
Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu Thr Leu Asn
                245                 250                 255
Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr Phe Glu Ala
            260                 265                 270
Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile Val Lys Asp
        275                 280                 285
Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His Pro Trp Leu
    290                 295                 300
Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg Leu Lys Ser
305                 310                 315                 320
Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp Lys Val Pro
                325                 330                 335
Leu Asp Ser Gly Lys Lys Glu Arg Glu Arg Glu Lys Glu Arg Lys Lys
            340                 345                 350
Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Lys Glu Gly Arg
        355                 360                 365
Lys Lys Glu Arg Lys Lys Glu Lys Glu Arg Lys Lys Lys Lys Glu Arg
    370                 375                 380
Lys Glu Gly Arg Lys Glu Gly Arg Lys Lys Glu Arg Lys Lys Glu Arg
385                 390                 395                 400
Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys
                405                 410
```

<210> 39
<211> 1239
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1239)
<223> MOOSE03350

<400> 39

```
agg aga cac aac ccc agg cag tgc gaa ctc ggt tat aag ctg ggc cgc   48
Arg Arg His Asn Pro Arg Gln Cys Glu Leu Gly Tyr Lys Leu Gly Arg
 1               5                  10                  15

aca att gga gag ggc agc tac tcc aag gtg aag gtg gcc aca tcc aag   96
Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys
            20                  25                  30

aag tac aag ggt acc gtg gcc atc aag gtg gtg gac cgg cgg cga gcg   144
Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
        35                  40                  45

ccc ccg gac ttc gtc aac aag ttc ctg ccg cga gag ctg tcc atc ctg   192
Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
    50                  55                  60

cgg ggc gtg cga cac ccg cac atc gtg cac gtc ttc gag ttc atc gag   240
Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
65                  70                  75                  80

gtg tgc aac ggg aaa ctg tac atc gtg atg gaa gcg gcc gcc acc gac   288
Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
                85                  90                  95

ctg ctg caa gcc gtg cag cgc aac ggg cgc atc ccc gga gtt cag gcg   336
Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
            100                 105                 110

cgc gac ctc ttt gcg cag atc gcc ggc gcc gtg cgc tac ctg cac gat   384
Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
        115                 120                 125

cat cac ctg gtg cac cgc gac ctc aag tgc gaa aac gtg ctg ctg agc   432
His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
    130                 135                 140

ccg gac gag cgc cgc gtc aag ctc acc gac ttc ggc ttc ggc cgc cag   480
Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
145                 150                 155                 160

gcc cat ggc tac cca gac ctg agc acc acc tac tgc ggc tca gcc gcc   528
Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Ala
                165                 170                 175

tac gcg tca ccc gag gtg ctc ctg ggc atc ccc tac gac ccc aag aag   576
Tyr Ala Ser Pro Glu Val Leu Leu Gly Ile Pro Tyr Asp Pro Lys Lys
            180                 185                 190

tac gat gtg tgg agc atg ggc gtc gtg ctc tac gtc atg gtc acc ggg   624
Tyr Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Val Thr Gly
        195                 200                 205

tgc atg ccc ttc gac gac tcg gac atc gcc ggc ctg ccc cgg cgc cag   672
Cys Met Pro Phe Asp Asp Ser Asp Ile Ala Gly Leu Pro Arg Arg Gln
    210                 215                 220

aaa cgc ggc gtg ctc tat ccc gaa ggc ctc gag ctg tcc gag cgc tgc   720
Lys Arg Gly Val Leu Tyr Pro Glu Gly Leu Glu Leu Ser Glu Arg Cys
225                 230                 235                 240
```

```
aag gcc ctg atc gcc gag ctg ctg cag ttc agc ccg tcc gcc agg ccc   768
Lys Ala Leu Ile Ala Glu Leu Leu Gln Phe Ser Pro Ser Ala Arg Pro
                245                 250                 255

tcc gcg ggc cag ggc tgc ctc ggc cat ccc tgc atc tgt cag tca aga   816
Ser Ala Gly Gln Gly Cys Leu Gly His Pro Cys Ile Cys Gln Ser Arg
            260                 265                 270

gag gtt tgc ccc gac agc ctg cgt ccc ctg cac cag gtc cca ttc cca   864
Glu Val Cys Pro Asp Ser Leu Arg Pro Leu His Gln Val Pro Phe Pro
        275                 280                 285

cct cgg aga agg aaa tgg agt tgt ttg ccg gga gct gcc cca agg ctg   912
Pro Arg Arg Arg Lys Trp Ser Cys Leu Pro Gly Ala Ala Pro Arg Leu
    290                 295                 300

ctg agg cag gag aat ggc atg aac ccc ggg ggg cag agc ctg cag gga   960
Leu Arg Gln Glu Asn Gly Met Asn Pro Gly Gly Gln Ser Leu Gln Gly
305                 310                 315                 320

gcc gag atc gtg cca ctg cgc act cca gcc tgg gcg aca gcc aga ctc   1008
Ala Glu Ile Val Pro Leu Arg Thr Pro Ala Trp Ala Thr Ala Arg Leu
                325                 330                 335

cgt ctc aaa aaa aaa aaa aaa aaa gaa aaa aaa aaa aag aaa aag aaa   1056
Arg Leu Lys Lys Lys Lys Lys Lys Glu Lys Lys Lys Lys Lys Lys Lys
            340                 345                 350

aat cct gtg aca gag aaa aag gac aca gtt atc aat gct act ttg agc   1104
Asn Pro Val Thr Glu Lys Lys Asp Thr Val Ile Asn Ala Thr Leu Ser
        355                 360                 365

ccc aaa gtg gcc aag gaa cac aca tcc cag cct gcc ccg tcc aga cca   1152
Pro Lys Val Ala Lys Glu His Thr Ser Gln Pro Ala Pro Ser Arg Pro
    370                 375                 380

tgg ggc agg cct ttg gtc caa gtg ctg ccc cct ccc aca gca gac aag   1200
Trp Gly Arg Pro Leu Val Gln Val Leu Pro Pro Pro Thr Ala Asp Lys
385                 390                 395                 400

cca ctc atg gta caa ggg gag gtg ggg aag aga aga gca               1239
Pro Leu Met Val Gln Gly Glu Val Gly Lys Arg Arg Ala
                405                 410
```

<210> 40
<211> 413
<212> PRT
<213> Homo sapiens

<400> 40

```
Arg Arg His Asn Pro Arg Gln Cys Glu Leu Gly Tyr Lys Leu Gly Arg
 1               5                  10                  15
Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys
            20                  25                  30
Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
        35                  40                  45
Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
    50                  55                  60
Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
65                  70                  75                  80
```

```
Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
                85                  90                  95
Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
            100                 105                 110
Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
        115                 120                 125
His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
    130                 135                 140
Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
145                 150                 155                 160
Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Ala
                165                 170                 175
Tyr Ala Ser Pro Glu Val Leu Leu Gly Ile Pro Tyr Asp Pro Lys Lys
            180                 185                 190
Tyr Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Val Thr Gly
        195                 200                 205
Cys Met Pro Phe Asp Asp Ser Asp Ile Ala Gly Leu Pro Arg Arg Gln
    210                 215                 220
Lys Arg Gly Val Leu Tyr Pro Glu Gly Leu Glu Leu Ser Glu Arg Cys
225                 230                 235                 240
Lys Ala Leu Ile Ala Glu Leu Leu Gln Phe Ser Pro Ser Ala Arg Pro
                245                 250                 255
Ser Ala Gly Gln Gly Cys Leu Gly His Pro Cys Ile Cys Gln Ser Arg
            260                 265                 270
Glu Val Cys Pro Asp Ser Leu Arg Pro Leu His Gln Val Pro Phe Pro
        275                 280                 285
Pro Arg Arg Arg Lys Trp Ser Cys Leu Pro Gly Ala Ala Pro Arg Leu
    290                 295                 300
Leu Arg Gln Glu Asn Gly Met Asn Pro Gly Gly Gln Ser Leu Gln Gly
305                 310                 315                 320
Ala Glu Ile Val Pro Leu Arg Thr Pro Ala Trp Ala Thr Ala Arg Leu
                325                 330                 335
Arg Leu Lys Lys Lys Lys Lys Lys Glu Lys Lys Lys Lys Lys Lys Lys
            340                 345                 350
Asn Pro Val Thr Glu Lys Lys Asp Thr Val Ile Asn Ala Thr Leu Ser
        355                 360                 365
Pro Lys Val Ala Lys Glu His Thr Ser Gln Pro Ala Pro Ser Arg Pro
    370                 375                 380
Trp Gly Arg Pro Leu Val Gln Val Leu Pro Pro Pro Thr Ala Asp Lys
385                 390                 395                 400
Pro Leu Met Val Gln Gly Glu Val Gly Lys Arg Arg Ala
                405                 410
```

<210> 41
<211> 2283
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2283)
<223> MOOSE03368

<400> 41

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agt ttg cgg gcc gcc ccg gga ccc cga cgc ccg tcg gcc gcc tcc tcc   48
Ser Leu Arg Ala Ala Pro Gly Pro Arg Arg Pro Ser Ala Ala Ser Ser
 1               5                  10                  15

tgt acc agc acc tgg ccc agc tgc gcc acc gcg cca gcc ccg gcg cac   96
Cys Thr Ser Thr Trp Pro Ser Cys Ala Thr Ala Pro Ala Pro Ala His
            20                  25                  30
```

```
gct ccc ggc ccg ggg ccc gcc agc gtc tcg cgc acc agc gcc cac agc   144
Ala Pro Gly Pro Gly Pro Ala Ser Val Ser Arg Thr Ser Ala His Ser
         35                  40                  45

tcg cgc tgc agg gcc tcg tac agc agc gcc acc cgc tca ctg ggt gcc   192
Ser Arg Cys Arg Ala Ser Tyr Ser Ser Ala Thr Arg Ser Leu Gly Ala
     50                  55                  60

cgt tgc cgg aac tcc atc gcc tcc tgt ccc gag gag cag ccc cac gtg   240
Arg Cys Arg Asn Ser Ile Ala Ser Cys Pro Glu Glu Gln Pro His Val
 65                  70                  75                  80

ggc aac tac cgc ctg ctg agg acc att ggg aag ggc aac ttt gcc aaa   288
Gly Asn Tyr Arg Leu Leu Arg Thr Ile Gly Lys Gly Asn Phe Ala Lys
                 85                  90                  95

gtc aag ctg gct cgg cac atc ctc act ggt cgg gag gtt gcc atc aag   336
Val Lys Leu Ala Arg His Ile Leu Thr Gly Arg Glu Val Ala Ile Lys
            100                 105                 110

att atc gac aaa acc cag ctg aat ccc agc agc ctg cag aag gat ccc   384
Ile Ile Asp Lys Thr Gln Leu Asn Pro Ser Ser Leu Gln Lys Asp Pro
        115                 120                 125

cca agc cac cca ccc tca ctc tcc tct gtc ttc ctt tct ggc cac gcc   432
Pro Ser His Pro Pro Ser Leu Ser Ser Val Phe Leu Ser Gly His Ala
    130                 135                 140

cag ctg ttc cga gaa gtc cgc atc atg aag ggc cta aac cac ccc aac   480
Gln Leu Phe Arg Glu Val Arg Ile Met Lys Gly Leu Asn His Pro Asn
145                 150                 155                 160

atc gtg aag ctc ttt gag gtg att gag act gag aag acg ctg tac ctg   528
Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu
                165                 170                 175

gtg atg gag tac gca agt gct gga gaa gtg ttt gac tac ctc gtg tcg   576
Val Met Glu Tyr Ala Ser Ala Gly Glu Val Phe Asp Tyr Leu Val Ser
            180                 185                 190

cat ggc cgc atg aag gag aag gaa gct cga gcc aag ttc cga cag att   624
His Gly Arg Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile
        195                 200                 205

gtt tcg gct gtg cac tat tgt cac cag aaa aat att gta cac agg gac   672
Val Ser Ala Val His Tyr Cys His Gln Lys Asn Ile Val His Arg Asp
    210                 215                 220

ctg aag gct gag aac ctc ttg ctg gat gcc gag gcc aac atc aag att   720
Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn Ile Lys Ile
225                 230                 235                 240

gct gac ttt ggc ttc agc aac gag ttc acg ctg gga tcg aag ctg gac   768
Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser Lys Leu Asp
                245                 250                 255

acg ttc tgc ggg agc ccc cca tat gcc gcc ccg gag ctg ttt cag ggc   816
Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly
            260                 265                 270
```

```
aag aag tac gac ggg ccg gag gtg gac atc tgg agc ctg gga gtc atc   864
Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Val Ile
        275                 280                 285

ctg tac acc ctc gtc agc ggc tcc ctg ccc ttc gac ggg cac aac ctc   912
Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly His Asn Leu
    290                 295                 300

aag gag ctg cgg gag cga gta ctc aga ggg aag tac cgg gtc cct ttc   960
Lys Glu Leu Arg Glu Arg Val Leu Arg Gly Lys Tyr Arg Val Pro Phe
305                 310                 315                 320

tac atg tca aca gac tgt gag agc atc ctg cgg aga ttt ttg gtg ctg   1008
Tyr Met Ser Thr Asp Cys Glu Ser Ile Leu Arg Arg Phe Leu Val Leu
                325                 330                 335

aac cca gct aaa cgc tgt act ctc gag caa atc atg aaa gac aaa tgg   1056
Asn Pro Ala Lys Arg Cys Thr Leu Glu Gln Ile Met Lys Asp Lys Trp
            340                 345                 350

atc aac atc ggc tat gag ggt gag gag ttg aag cca tac aca gag ccc   1104
Ile Asn Ile Gly Tyr Glu Gly Glu Glu Leu Lys Pro Tyr Thr Glu Pro
        355                 360                 365

gag gag gac ttc ggg gac acc aag aga att gag gtg atg gtg ggt atg   1152
Glu Glu Asp Phe Gly Asp Thr Lys Arg Ile Glu Val Met Val Gly Met
    370                 375                 380

ggc tac aca cgg gaa gaa atc aaa gag tcc ttg acc agc cag aag tac   1200
Gly Tyr Thr Arg Glu Glu Ile Lys Glu Ser Leu Thr Ser Gln Lys Tyr
385                 390                 395                 400

aac gaa gtg acc gcc acc tac ctc ctg ctg ggc agg aag act gag cga   1248
Asn Glu Val Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys Thr Glu Arg
                405                 410                 415

cac cac caa cgg aac aag ttc cag caa agg cac cag cca cag caa agg   1296
His His Gln Arg Asn Lys Phe Gln Gln Arg His Gln Pro Gln Gln Arg
            420                 425                 430

gca gcg gaa tcg cac cac tgc act cca gcc tgg caa cag aac cag act   1344
Ala Ala Glu Ser His His Cys Thr Pro Ala Trp Gln Gln Asn Gln Thr
        435                 440                 445

ttg tct caa aaa aaa aaa aaa aaa aaa gaa ggt ggc cca tcc cct gca   1392
Leu Ser Gln Lys Lys Lys Lys Lys Lys Glu Gly Gly Pro Ser Pro Ala
    450                 455                 460

ccc ctg cac ccc aaa cgc agc ccg acg agc acg ggg gag gcg gag ctg   1440
Pro Leu His Pro Lys Arg Ser Pro Thr Ser Thr Gly Glu Ala Glu Leu
465                 470                 475                 480

aag gag gag cgg ctg cca ggc cgg aag gcg agc tgc agc acc gcg ggg   1488
Lys Glu Glu Arg Leu Pro Gly Arg Lys Ala Ser Cys Ser Thr Ala Gly
                485                 490                 495

agt ggg agt cga ggg ctg ccc ccc tcc agc ccc atg gtc agc agc gcc   1536
Ser Gly Ser Arg Gly Leu Pro Pro Ser Ser Pro Met Val Ser Ser Ala
            500                 505                 510
```

```
cac aac ccc aac aag gca gag atc cca gag cgg cgg aag gac agc acg   1584
His Asn Pro Asn Lys Ala Glu Ile Pro Glu Arg Arg Lys Asp Ser Thr
        515                 520                 525

agc acc ccc gaa tgt gaa gaa tca aag gga ctg ggg ccc tgg cct gcc   1632
Ser Thr Pro Glu Cys Glu Glu Ser Lys Gly Leu Gly Pro Trp Pro Ala
    530                 535                 540

tca gtc ccc cac cct gac ttg tct gtc tct gcc cac agc tca ggc acc   1680
Ser Val Pro His Pro Asp Leu Ser Val Ser Ala His Ser Ser Gly Thr
545                 550                 555                 560

cca cgg gtg ccc cct gcc tcc ccc tcc agt cac agc ctg gca ccc cca   1728
Pro Arg Val Pro Pro Ala Ser Pro Ser Ser His Ser Leu Ala Pro Pro
                565                 570                 575

tca ggg gag cgg agc cgc ctg gca cgt ggt tcc acc atc cgc agc acc   1776
Ser Gly Glu Arg Ser Arg Leu Ala Arg Gly Ser Thr Ile Arg Ser Thr
            580                 585                 590

ttc cat ggt ggc cag gtc cgg gac cgg cgg gca ggg ggt ggg ggt ggt   1824
Phe His Gly Gly Gln Val Arg Asp Arg Arg Ala Gly Gly Gly Gly Gly
        595                 600                 605

ggg ggt gtg cag aat ggg ccc cct gcc tct ccc aca ctg gcc cat gag   1872
Gly Gly Val Gln Asn Gly Pro Pro Ala Ser Pro Thr Leu Ala His Glu
    610                 615                 620

gct gca ccc ctg ccc gcc ggg cgg ccc cgc ccc acc acc aac ctc ttc   1920
Ala Ala Pro Leu Pro Ala Gly Arg Pro Arg Pro Thr Thr Asn Leu Phe
625                 630                 635                 640

acc aag ctg acc tcc aaa ctg acc cga agt tgc cat cta cct tgg gat   1968
Thr Lys Leu Thr Ser Lys Leu Thr Arg Ser Cys His Leu Pro Trp Asp
                645                 650                 655

caa acg gaa acc gcc ccc cgg ctg ctc cga ttc ccc tgg agt gtg aag   2016
Gln Thr Glu Thr Ala Pro Arg Leu Leu Arg Phe Pro Trp Ser Val Lys
            660                 665                 670

ctg acc agc tcg cgc cct cct gag gcc ctg atg gca gct ctg cgc cag   2064
Leu Thr Ser Ser Arg Pro Pro Glu Ala Leu Met Ala Ala Leu Arg Gln
        675                 680                 685

gcc aca gca gcc gcc cgc tgc cgc tgc cgc cag cca cag ccg ttc ctg   2112
Ala Thr Ala Ala Ala Arg Cys Arg Cys Arg Gln Pro Gln Pro Phe Leu
    690                 695                 700

ctg gcc tgc ctg cac ggg ggt gcg ggc ggg ccc gag ccc ctg tcc cac   2160
Leu Ala Cys Leu His Gly Gly Ala Gly Gly Pro Glu Pro Leu Ser His
705                 710                 715                 720

ttc gaa gtg gag gtc tgc cag ctg ccc cgg cca ggc ttg cgg gga gtt   2208
Phe Glu Val Glu Val Cys Gln Leu Pro Arg Pro Gly Leu Arg Gly Val
                725                 730                 735

ctc ttc cgc cgt gtg gcg ggc acc gcc ctg gcc ttc cgc acc ctc gtc   2256
Leu Phe Arg Arg Val Ala Gly Thr Ala Leu Ala Phe Arg Thr Leu Val
            740                 745                 750
```

```
acc cgc atc tcc aac gac ctc gag ctc                                    2283
Thr Arg Ile Ser Asn Asp Leu Glu Leu
        755                 760
```

<210> 42
<211> 761
<212> PRT
<213> Homo sapiens

<400> 42

```
Ser Leu Arg Ala Ala Pro Gly Pro Arg Arg Pro Ser Ala Ala Ser Ser
 1               5                  10                  15
Cys Thr Ser Thr Trp Pro Ser Cys Ala Thr Ala Pro Ala Pro Ala His
            20                  25                  30
Ala Pro Gly Pro Gly Pro Ala Ser Val Ser Arg Thr Ser Ala His Ser
        35                  40                  45
Ser Arg Cys Arg Ala Ser Tyr Ser Ser Ala Thr Arg Ser Leu Gly Ala
    50                  55                  60
Arg Cys Arg Asn Ser Ile Ala Ser Cys Pro Glu Glu Gln Pro His Val
65                  70                  75                  80
Gly Asn Tyr Arg Leu Leu Arg Thr Ile Gly Lys Gly Asn Phe Ala Lys
                85                  90                  95
Val Lys Leu Ala Arg His Ile Leu Thr Gly Arg Glu Val Ala Ile Lys
            100                 105                 110
Ile Ile Asp Lys Thr Gln Leu Asn Pro Ser Ser Leu Gln Lys Asp Pro
        115                 120                 125
Pro Ser His Pro Pro Ser Leu Ser Ser Val Phe Leu Ser Gly His Ala
    130                 135                 140
Gln Leu Phe Arg Glu Val Arg Ile Met Lys Gly Leu Asn His Pro Asn
145                 150                 155                 160
Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu
                165                 170                 175
Val Met Glu Tyr Ala Ser Ala Gly Glu Val Phe Asp Tyr Leu Val Ser
            180                 185                 190
His Gly Arg Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile
        195                 200                 205
Val Ser Ala Val His Tyr Cys His Gln Lys Asn Ile Val His Arg Asp
    210                 215                 220
Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn Ile Lys Ile
225                 230                 235                 240
Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser Lys Leu Asp
                245                 250                 255
Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly
            260                 265                 270
Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Val Ile
        275                 280                 285
Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly His Asn Leu
    290                 295                 300
Lys Glu Leu Arg Glu Arg Val Leu Arg Gly Lys Tyr Arg Val Pro Phe
305                 310                 315                 320
Tyr Met Ser Thr Asp Cys Glu Ser Ile Leu Arg Arg Phe Leu Val Leu
                325                 330                 335
Asn Pro Ala Lys Arg Cys Thr Leu Glu Gln Ile Met Lys Asp Lys Trp
            340                 345                 350
Ile Asn Ile Gly Tyr Glu Gly Glu Glu Leu Lys Pro Tyr Thr Glu Pro
        355                 360                 365
Glu Glu Asp Phe Gly Asp Thr Lys Arg Ile Glu Val Met Val Gly Met
    370                 375                 380
Gly Tyr Thr Arg Glu Glu Ile Lys Glu Ser Leu Thr Ser Gln Lys Tyr
385                 390                 395                 400
```

```
Asn Glu Val Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys Thr Glu Arg
                405                 410                 415
His His Gln Arg Asn Lys Phe Gln Gln Arg His Gln Pro Gln Gln Arg
            420                 425                 430
Ala Ala Glu Ser His His Cys Thr Pro Ala Trp Gln Gln Asn Gln Thr
        435                 440                 445
Leu Ser Gln Lys Lys Lys Lys Lys Lys Glu Gly Gly Pro Ser Pro Ala
    450                 455                 460
Pro Leu His Pro Lys Arg Ser Pro Thr Ser Thr Gly Glu Ala Glu Leu
465                 470                 475                 480
Lys Glu Glu Arg Leu Pro Gly Arg Lys Ala Ser Cys Ser Thr Ala Gly
                485                 490                 495
Ser Gly Ser Arg Gly Leu Pro Pro Ser Ser Pro Met Val Ser Ser Ala
            500                 505                 510
His Asn Pro Asn Lys Ala Glu Ile Pro Glu Arg Arg Lys Asp Ser Thr
        515                 520                 525
Ser Thr Pro Glu Cys Glu Glu Ser Lys Gly Leu Gly Pro Trp Pro Ala
    530                 535                 540
Ser Val Pro His Pro Asp Leu Ser Val Ser Ala His Ser Ser Gly Thr
545                 550                 555                 560
Pro Arg Val Pro Pro Ala Ser Pro Ser Ser His Ser Leu Ala Pro Pro
                565                 570                 575
Ser Gly Glu Arg Ser Arg Leu Ala Arg Gly Ser Thr Ile Arg Ser Thr
            580                 585                 590
Phe His Gly Gly Gln Val Arg Asp Arg Arg Ala Gly Gly Gly Gly Gly
        595                 600                 605
Gly Gly Val Gln Asn Gly Pro Pro Ala Ser Pro Thr Leu Ala His Glu
    610                 615                 620
Ala Ala Pro Leu Pro Ala Gly Arg Pro Arg Pro Thr Thr Asn Leu Phe
625                 630                 635                 640
Thr Lys Leu Thr Ser Lys Leu Thr Arg Ser Cys His Leu Pro Trp Asp
                645                 650                 655
Gln Thr Glu Thr Ala Pro Arg Leu Leu Arg Phe Pro Trp Ser Val Lys
            660                 665                 670
Leu Thr Ser Ser Arg Pro Pro Glu Ala Leu Met Ala Ala Leu Arg Gln
        675                 680                 685
Ala Thr Ala Ala Ala Arg Cys Arg Cys Arg Gln Pro Gln Pro Phe Leu
    690                 695                 700
Leu Ala Cys Leu His Gly Gly Ala Gly Gly Pro Glu Pro Leu Ser His
705                 710                 715                 720
Phe Glu Val Glu Val Cys Gln Leu Pro Arg Pro Gly Leu Arg Gly Val
                725                 730                 735
Leu Phe Arg Arg Val Ala Gly Thr Ala Leu Ala Phe Arg Thr Leu Val
            740                 745                 750
Thr Arg Ile Ser Asn Asp Leu Glu Leu
        755                 760
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<211> 3234
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<213> Homo sapiens

<220>
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<222> (1)...(3234)
<223> MOOSE03372

<400> 43

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Met Gly Arg Pro Gly Tyr Gly Ser Arg Ser His His Thr Pro Thr Ala
 1               5                  10                  15
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```
tct ccg gcc agc tgt gca aaa agg aac gcg tcc tcc ctg ggc cca cgg   96
Ser Pro Ala Ser Cys Ala Lys Arg Asn Ala Ser Ser Leu Gly Pro Arg
            20                  25                  30

ctg ggt ggc cac aca gag caa gac tcc gtc tca gga aaa aga aaa aaa   144
Leu Gly Gly His Thr Glu Gln Asp Ser Val Ser Gly Lys Arg Lys Lys
        35                  40                  45

aga aaa aag aaa cgg agg ccc agg ctg atg ata tca ccg cca ggg gtg   192
Arg Lys Lys Lys Arg Arg Pro Arg Leu Met Ile Ser Pro Pro Gly Val
    50                  55                  60

ccc agc agg gac agt cgg agc agg gct gtg agc cgg ggt cag ggc cag   240
Pro Ser Arg Asp Ser Arg Ser Arg Ala Val Ser Arg Gly Gln Gly Gln
65                  70                  75                  80

cag aag ccc ctc cgg gtg ggt ttt tac gac atc gag cgg acc ctg ggc   288
Gln Lys Pro Leu Arg Val Gly Phe Tyr Asp Ile Glu Arg Thr Leu Gly
                85                  90                  95

aaa ggc aac ttc gcg gtg gtg aag ctg gcg cgg cat cga gtc acc aaa   336
Lys Gly Asn Phe Ala Val Val Lys Leu Ala Arg His Arg Val Thr Lys
            100                 105                 110

acg cag gtt gca ata aaa ata att gat aaa aca cga tta gat tca agc   384
Thr Gln Val Ala Ile Lys Ile Ile Asp Lys Thr Arg Leu Asp Ser Ser
        115                 120                 125

aat ttg gag aaa atc tat cgt gag gtt cag ctg atg aag ctt ctg aac   432
Asn Leu Glu Lys Ile Tyr Arg Glu Val Gln Leu Met Lys Leu Leu Asn
    130                 135                 140

cat cca cac atc ata aag ctt tac cag gtt atg gaa aca aag gac atg   480
His Pro His Ile Ile Lys Leu Tyr Gln Val Met Glu Thr Lys Asp Met
145                 150                 155                 160

ctt tac atc gtc act gaa ttt gct aaa aat gga gaa atg ttt gat tat   528
Leu Tyr Ile Val Thr Glu Phe Ala Lys Asn Gly Glu Met Phe Asp Tyr
                165                 170                 175

ttg act tcc aac ggg cac ctg agt gag aac gag gcg cgg aag aag ttc   576
Leu Thr Ser Asn Gly His Leu Ser Glu Asn Glu Ala Arg Lys Lys Phe
            180                 185                 190

tgg caa atc ctg tcg gcc gtg gag tac tgt cac gac cat cac atc gtc   624
Trp Gln Ile Leu Ser Ala Val Glu Tyr Cys His Asp His His Ile Val
        195                 200                 205

cac cgg gac ctc aag acc gag aac ctc ctg ctg gat ggc aac atg gac   672
His Arg Asp Leu Lys Thr Glu Asn Leu Leu Leu Asp Gly Asn Met Asp
    210                 215                 220

atc aag ctg gca ggc acg gag gat ttt gga ttt ggg aat ttc tac aag   720
Ile Lys Leu Ala Gly Thr Glu Asp Phe Gly Phe Gly Asn Phe Tyr Lys
225                 230                 235                 240

tca gga gag cct ctg tcc acg tgg tgt ggg agc ccc ccg tat gcc gcc   768
Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly Ser Pro Pro Tyr Ala Ala
                245                 250                 255
```

```
ccg gaa gtc ttt gag ggg aag gag tat gaa ggc ccc cag ctg gac atc   816
Pro Glu Val Phe Glu Gly Lys Glu Tyr Glu Gly Pro Gln Leu Asp Ile
            260                 265                 270

tgg agc ctg ggc gtg gtg ctg tac gtc ctg gtc tgc ggt tct ctc ccc   864
Trp Ser Leu Gly Val Val Leu Tyr Val Leu Val Cys Gly Ser Leu Pro
        275                 280                 285

ttc gat ggg cct aac ctg ccg acg ctg aga cag cgg gtg ctg gag ggc   912
Phe Asp Gly Pro Asn Leu Pro Thr Leu Arg Gln Arg Val Leu Glu Gly
    290                 295                 300

cgc ttc cgc atc ccc ttc ttc atg tct caa gac tgt gag agc ctg atc   960
Arg Phe Arg Ile Pro Phe Phe Met Ser Gln Asp Cys Glu Ser Leu Ile
305                 310                 315                 320

cgc cgc atg ctg gtg gtg gac ccc gcc agg cgc atc acc atc gcc cag   1008
Arg Arg Met Leu Val Val Asp Pro Ala Arg Arg Ile Thr Ile Ala Gln
                325                 330                 335

atc cgg cag cac cgg tgg atg cgg gct gag ccc tgc ttg ccg gga ccc   1056
Ile Arg Gln His Arg Trp Met Arg Ala Glu Pro Cys Leu Pro Gly Pro
            340                 345                 350

gcc tgc ccc gcc ttc tcc gca cac agc tac acc tcc aac ctg ggc gac   1104
Ala Cys Pro Ala Phe Ser Ala His Ser Tyr Thr Ser Asn Leu Gly Asp
        355                 360                 365

tac gat gag cag gcg ctg ggt atc atg cag acc ctg ggc gtg gac cgg   1152
Tyr Asp Glu Gln Ala Leu Gly Ile Met Gln Thr Leu Gly Val Asp Arg
    370                 375                 380

cag agg acg gtg gag tca ctg caa aac agc agc tat aac cac ttt gct   1200
Gln Arg Thr Val Glu Ser Leu Gln Asn Ser Ser Tyr Asn His Phe Ala
385                 390                 395                 400

gcc att tat tac ctc ctc ctt gag cgg ctc aag gag tat cgg aat gcc   1248
Ala Ile Tyr Tyr Leu Leu Leu Glu Arg Leu Lys Glu Tyr Arg Asn Ala
                405                 410                 415

cag tgc gcc cgc ccc ggg cct gcc agg cag ccg cgg cct cgg agc tcg   1296
Gln Cys Ala Arg Pro Gly Pro Ala Arg Gln Pro Arg Pro Arg Ser Ser
            420                 425                 430

gac ctc agt ggt ttg gag gtg agg ggg agg agt ctc ctc cca ggc ccc   1344
Asp Leu Ser Gly Leu Glu Val Arg Gly Arg Ser Leu Leu Pro Gly Pro
        435                 440                 445

agg ctc cct ccc ctg tca ggc acc ggc ttg gag ggc gga ctg gcc tct   1392
Arg Leu Pro Pro Leu Ser Gly Thr Gly Leu Glu Gly Gly Leu Ala Ser
    450                 455                 460

cgg ggt ggg ggt ggg gag aga ggg gat gcc cca gcc aga ggg agg tcc   1440
Arg Gly Gly Gly Gly Glu Arg Gly Asp Ala Pro Ala Arg Gly Arg Ser
465                 470                 475                 480

ctg ggc cca gcc tgg agg gag ccg agg caa gat cca cct aat tgt gat   1488
Leu Gly Pro Ala Trp Arg Glu Pro Arg Gln Asp Pro Pro Asn Cys Asp
                485                 490                 495
```

```
gga atg aat ttc ggc agc cac agg aaa cta aga agc cca aac acg ccg   1536
Gly Met Asn Phe Gly Ser His Arg Lys Leu Arg Ser Pro Asn Thr Pro
            500                 505                 510

gtt cct atc cgt gaa gga caa aag acc cac gcg ttg agt cac cag ggc   1584
Val Pro Ile Arg Glu Gly Gln Lys Thr His Ala Leu Ser His Gln Gly
        515                 520                 525

tat cag gga aga gcc tgg gcc ggg gtc cta gcc cca gag ccc aga atc   1632
Tyr Gln Gly Arg Ala Trp Ala Gly Val Leu Ala Pro Glu Pro Arg Ile
    530                 535                 540

ccc gct tcc agt tct cag ctg ccc cgt gag cgg gct gtc agc aac tcc   1680
Pro Ala Ser Ser Ser Gln Leu Pro Arg Glu Arg Ala Val Ser Asn Ser
545                 550                 555                 560

cag cag cca ggc ctg tgg gct gag atg gtg gcg gtt tcc tgc cct gcc   1728
Gln Gln Pro Gly Leu Trp Ala Glu Met Val Ala Val Ser Cys Pro Ala
                565                 570                 575

tct cct ccc ctc cgg ggt cag ggg gct cct ctc ctg acc ttg tac tta   1776
Ser Pro Pro Leu Arg Gly Gln Gly Ala Pro Leu Leu Thr Leu Tyr Leu
            580                 585                 590

gaa acg aca cag ccc cat ggg ctg tgg gca tcc tcc agc cgg tgt ccc   1824
Glu Thr Thr Gln Pro His Gly Leu Trp Ala Ser Ser Ser Arg Cys Pro
        595                 600                 605

atc tgc cct gca agc agt gcc tgg gct cag agc agc cca cag gac act   1872
Ile Cys Pro Ala Ser Ser Ala Trp Ala Gln Ser Ser Pro Gln Asp Thr
    610                 615                 620

gtc caa gat gcg cag acc ccg agg gcc aga ggg acc ggc tct gca gga   1920
Val Gln Asp Ala Gln Thr Pro Arg Ala Arg Gly Thr Gly Ser Ala Gly
625                 630                 635                 640

atc cca cct cct ggg ccc act ccg cac aga gtg ttc tgc agg gcc tgg   1968
Ile Pro Pro Pro Gly Pro Thr Pro His Arg Val Phe Cys Arg Ala Trp
                645                 650                 655

gag aac cag gca cct ggc cag gac agc ctg tgg gtg ggc agc cgt gtg   2016
Glu Asn Gln Ala Pro Gly Gln Asp Ser Leu Trp Val Gly Ser Arg Val
            660                 665                 670

cac aga tac aca cac acg tca ggg aca gac aca cac aca cca ggg aca   2064
His Arg Tyr Thr His Thr Ser Gly Thr Asp Thr His Thr Pro Gly Thr
        675                 680                 685

cac acc aca cac acc agg gac gca cac cac aca cac cag gga cac cca   2112
His Thr Thr His Thr Arg Asp Ala His His Thr His Gln Gly His Pro
    690                 695                 700

cac aca cca cgg acg cac acc aca cac acc agg gac acc cac aca cac   2160
His Thr Pro Arg Thr His Thr Thr His Thr Arg Asp Thr His Thr His
705                 710                 715                 720

cag gga cgc aca cca cac aca cca ggg acc cct gca cac acc agg gac   2208
Gln Gly Arg Thr Pro His Thr Pro Gly Thr Pro Ala His Thr Arg Asp
                725                 730                 735
```

```
aca cac aca cac acc ggg gat gca cac cac aca cac acc agg gat gca   2256
Thr His Thr His Thr Gly Asp Ala His His Thr His Thr Arg Asp Ala
            740                 745                 750

tac cac aca cac cag gga ccc aca cac aca cca ggg acc cac aca cac   2304
Tyr His Thr His Gln Gly Pro Thr His Thr Pro Gly Thr His Thr His
        755                 760                 765

tcc agg gac gca cac cac aca cac cag gga ccc ccg caa aca cac aca   2352
Ser Arg Asp Ala His His Thr His Gln Gly Pro Pro Gln Thr His Thr
    770                 775                 780

cca ggg aca cac aca cac cag gga cac aca cac cac aca cac acc agg   2400
Pro Gly Thr His Thr His Gln Gly His Thr His His Thr His Thr Arg
785                 790                 795                 800

gac aca cac cac aca cac cag gga cac aca cca ggg aca gac aca caa   2448
Asp Thr His His Thr His Gln Gly His Thr Pro Gly Thr Asp Thr Gln
                805                 810                 815

ggg atg cac aca cac cag gga cgc aca gca cac aca cca ggg acc cat   2496
Gly Met His Thr His Gln Gly Arg Thr Ala His Thr Pro Gly Thr His
            820                 825                 830

aca cac acc agg gat gca cac aca tca ggg aca cac aaa cac cag gga   2544
Thr His Thr Arg Asp Ala His Thr Ser Gly Thr His Lys His Gln Gly
        835                 840                 845

cgc aca cca cac aca cca ggg aca cac acc aca cac aca cac acc atg   2592
Arg Thr Pro His Thr Pro Gly Thr His Thr Thr His Thr His Thr Met
    850                 855                 860

gac aca cac acc act ggt aca cgt tgt gaa cac acc atg gac aca cag   2640
Asp Thr His Thr Thr Gly Thr Arg Cys Glu His Thr Met Asp Thr Gln
865                 870                 875                 880

aga aac aca cac aac atg ggt aca cac aat aca cac cac aaa gac ata   2688
Arg Asn Thr His Asn Met Gly Thr His Asn Thr His His Lys Asp Ile
                885                 890                 895

acc tcc cca cac act cac ata cat aac aca cat acc aga gac aca tgg   2736
Thr Ser Pro His Thr His Ile His Asn Thr His Thr Arg Asp Thr Trp
            900                 905                 910

tta cac aca gca cac act ccc tca tca gac acc cac aca cca tct cac   2784
Leu His Thr Ala His Thr Pro Ser Ser Asp Thr His Thr Pro Ser His
        915                 920                 925

aca cac cac aca ccc atc aga cac cca cac atc atc tca cac acc aca   2832
Thr His His Thr Pro Ile Arg His Pro His Ile Ile Ser His Thr Thr
    930                 935                 940

cac tca cca gac acc cac aca tca tct cac aca cac cac aca ccc atc   2880
His Ser Pro Asp Thr His Thr Ser Ser His Thr His His Thr Pro Ile
945                 950                 955                 960

aga cac cca aca tca tct cac aca cac tac aca ctc acc aga cac cca   2928
Arg His Pro Thr Ser Ser His Thr His Tyr Thr Leu Thr Arg His Pro
                965                 970                 975
```

```
cac atc atc tcg cac aca cca cac acc cat cag aca ccc aac atc atc   2976
His Ile Ile Ser His Thr Pro His Thr His Gln Thr Pro Asn Ile Ile
            980                 985                 990

tca cag cag tca tat gca caa tta gag ggg gct tct cct agc ctg tgt   3024
Ser Gln Gln Ser Tyr Ala Gln Leu Glu Gly Ala Ser Pro Ser Leu Cys
        995                 1000                1005

tct cct cgg cat ccc tgg tgg ctt ggg gct ggg gag gga cac cca gct   3072
Ser Pro Arg His Pro Trp Trp Leu Gly Ala Gly Glu Gly His Pro Ala
    1010                1015                1020

cct ccc gac cga cgt cta tgg ctt ctg gtg ctc cac tct cct ctc gga   3120
Pro Pro Asp Arg Arg Leu Trp Leu Leu Val Leu His Ser Pro Leu Gly
1025                1030                1035                1040

cag cag caa aca ttt aag atg gac ata gca gaa aga agg gag ccg gcc   3168
Gln Gln Gln Thr Phe Lys Met Asp Ile Ala Glu Arg Arg Glu Pro Ala
                1045                1050                1055

atg tgc tcc cag caa aac cca aat gcc cgg ttc cct ctc tgc tcc tct   3216
Met Cys Ser Gln Gln Asn Pro Asn Ala Arg Phe Pro Leu Cys Ser Ser
            1060                1065                1070

ctc gct cct ctc cca ctc                                          3234
Leu Ala Pro Leu Pro Leu
        1075
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<210> 44
<211> 1078
<212> PRT
<213> Homo sapiens

<400> 44

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Met Gly Arg Pro Gly Tyr Gly Ser Arg Ser His His Thr Pro Thr Ala
 1               5                  10                  15
Ser Pro Ala Ser Cys Ala Lys Arg Asn Ala Ser Ser Leu Gly Pro Arg
            20                  25                  30
Leu Gly Gly His Thr Glu Gln Asp Ser Val Ser Gly Lys Arg Lys Lys
        35                  40                  45
Arg Lys Lys Lys Arg Arg Pro Arg Leu Met Ile Ser Pro Pro Gly Val
    50                  55                  60
Pro Ser Arg Asp Ser Arg Ser Arg Ala Val Ser Arg Gly Gln Gly Gln
65                  70                  75                  80
Gln Lys Pro Leu Arg Val Gly Phe Tyr Asp Ile Glu Arg Thr Leu Gly
                85                  90                  95
Lys Gly Asn Phe Ala Val Val Lys Leu Ala Arg His Arg Val Thr Lys
            100                 105                 110
Thr Gln Val Ala Ile Lys Ile Ile Asp Lys Thr Arg Leu Asp Ser Ser
        115                 120                 125
Asn Leu Glu Lys Ile Tyr Arg Glu Val Gln Leu Met Lys Leu Leu Asn
    130                 135                 140
His Pro His Ile Ile Lys Leu Tyr Gln Val Met Glu Thr Lys Asp Met
145                 150                 155                 160
Leu Tyr Ile Val Thr Glu Phe Ala Lys Asn Gly Glu Met Phe Asp Tyr
                165                 170                 175
Leu Thr Ser Asn Gly His Leu Ser Glu Asn Glu Ala Arg Lys Lys Phe
            180                 185                 190
Trp Gln Ile Leu Ser Ala Val Glu Tyr Cys His Asp His His Ile Val
        195                 200                 205
```

```
His Arg Asp Leu Lys Thr Glu Asn Leu Leu Leu Asp Gly Asn Met Asp
    210                 215                 220
Ile Lys Leu Ala Gly Thr Glu Asp Phe Gly Phe Gly Asn Phe Tyr Lys
225                 230                 235                 240
Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly Ser Pro Pro Tyr Ala Ala
                245                 250                 255
Pro Glu Val Phe Glu Gly Lys Glu Tyr Glu Gly Pro Gln Leu Asp Ile
            260                 265                 270
Trp Ser Leu Gly Val Val Leu Tyr Val Leu Val Cys Gly Ser Leu Pro
        275                 280                 285
Phe Asp Gly Pro Asn Leu Pro Thr Leu Arg Gln Arg Val Leu Glu Gly
    290                 295                 300
Arg Phe Arg Ile Pro Phe Phe Met Ser Gln Asp Cys Glu Ser Leu Ile
305                 310                 315                 320
Arg Arg Met Leu Val Val Asp Pro Ala Arg Arg Ile Thr Ile Ala Gln
                325                 330                 335
Ile Arg Gln His Arg Trp Met Arg Ala Glu Pro Cys Leu Pro Gly Pro
            340                 345                 350
Ala Cys Pro Ala Phe Ser Ala His Ser Tyr Thr Ser Asn Leu Gly Asp
        355                 360                 365
Tyr Asp Glu Gln Ala Leu Gly Ile Met Gln Thr Leu Gly Val Asp Arg
    370                 375                 380
Gln Arg Thr Val Glu Ser Leu Gln Asn Ser Ser Tyr Asn His Phe Ala
385                 390                 395                 400
Ala Ile Tyr Tyr Leu Leu Leu Glu Arg Leu Lys Glu Tyr Arg Asn Ala
                405                 410                 415
Gln Cys Ala Arg Pro Gly Pro Ala Arg Gln Pro Arg Pro Arg Ser Ser
            420                 425                 430
Asp Leu Ser Gly Leu Glu Val Arg Gly Arg Ser Leu Leu Pro Gly Pro
        435                 440                 445
Arg Leu Pro Pro Leu Ser Gly Thr Gly Leu Glu Gly Gly Leu Ala Ser
    450                 455                 460
Arg Gly Gly Gly Gly Glu Arg Gly Asp Ala Pro Ala Arg Gly Arg Ser
465                 470                 475                 480
Leu Gly Pro Ala Trp Arg Glu Pro Arg Gln Asp Pro Pro Asn Cys Asp
                485                 490                 495
Gly Met Asn Phe Gly Ser His Arg Lys Leu Arg Ser Pro Asn Thr Pro
            500                 505                 510
Val Pro Ile Arg Glu Gly Gln Lys Thr His Ala Leu Ser His Gln Gly
        515                 520                 525
Tyr Gln Gly Arg Ala Trp Ala Gly Val Leu Ala Pro Glu Pro Arg Ile
    530                 535                 540
Pro Ala Ser Ser Ser Gln Leu Pro Arg Glu Arg Ala Val Ser Asn Ser
545                 550                 555                 560
Gln Gln Pro Gly Leu Trp Ala Glu Met Val Ala Val Ser Cys Pro Ala
                565                 570                 575
Ser Pro Pro Leu Arg Gly Gln Gly Ala Pro Leu Leu Thr Leu Tyr Leu
            580                 585                 590
Glu Thr Thr Gln Pro His Gly Leu Trp Ala Ser Ser Ser Arg Cys Pro
        595                 600                 605
Ile Cys Pro Ala Ser Ser Ala Trp Ala Gln Ser Ser Pro Gln Asp Thr
    610                 615                 620
Val Gln Asp Ala Gln Thr Pro Arg Ala Arg Gly Thr Gly Ser Ala Gly
625                 630                 635                 640
Ile Pro Pro Pro Gly Pro Thr Pro His Arg Val Phe Cys Arg Ala Trp
                645                 650                 655
Glu Asn Gln Ala Pro Gly Gln Asp Ser Leu Trp Val Gly Ser Arg Val
            660                 665                 670
His Arg Tyr Thr His Thr Ser Gly Thr Asp Thr His Thr Pro Gly Thr
        675                 680                 685
His Thr Thr His Thr Arg Asp Ala His His Thr His Gln Gly His Pro
    690                 695                 700
```

His Thr Pro Arg Thr His Thr Thr His Thr Arg Asp Thr His Thr His
705 710 715 720
Gln Gly Arg Thr Pro His Thr Pro Gly Thr Pro Ala His Thr Arg Asp
725 730 735
Thr His Thr His Thr Gly Asp Ala His His Thr His Thr Arg Asp Ala
740 745 750
Tyr His Thr His Gln Gly Pro Thr His Thr Pro Gly Thr His Thr His
755 760 765
Ser Arg Asp Ala His His Thr His Gln Gly Pro Pro Gln Thr His Thr
770 775 780
Pro Gly Thr His Thr His Gln Gly His Thr His His Thr His Thr Arg
785 790 795 800
Asp Thr His His Thr His Gln Gly His Thr Pro Gly Thr Asp Thr Gln
805 810 815
Gly Met His Thr His Gln Gly Arg Thr Ala His Thr Pro Gly Thr His
820 825 830
Thr His Thr Arg Asp Ala His Thr Ser Gly Thr His Lys His Gln Gly
835 840 845
Arg Thr Pro His Thr Pro Gly Thr His Thr Thr His Thr His Thr Met
850 855 860
Asp Thr His Thr Thr Gly Thr Arg Cys Glu His Thr Met Asp Thr Gln
865 870 875 880
Arg Asn Thr His Asn Met Gly Thr His Asn Thr His His Lys Asp Ile
885 890 895
Thr Ser Pro His Thr His Ile His Asn Thr His Thr Arg Asp Thr Trp
900 905 910
Leu His Thr Ala His Thr Pro Ser Ser Asp Thr His Thr Pro Ser His
915 920 925
Thr His His Thr Pro Ile Arg His Pro His Ile Ile Ser His Thr Thr
930 935 940
His Ser Pro Asp Thr His Thr Ser Ser His Thr His His Thr Pro Ile
945 950 955 960
Arg His Pro Thr Ser Ser His Thr His Tyr Thr Leu Thr Arg His Pro
965 970 975
His Ile Ile Ser His Thr Pro His Thr His Gln Thr Pro Asn Ile Ile
980 985 990
Ser Gln Gln Ser Tyr Ala Gln Leu Glu Gly Ala Ser Pro Ser Leu Cys
995 1000 1005
Ser Pro Arg His Pro Trp Trp Leu Gly Ala Gly Glu Gly His Pro Ala
1010 1015 1020
Pro Pro Asp Arg Arg Leu Trp Leu Leu Val Leu His Ser Pro Leu Gly
1025 1030 1035 1040
Gln Gln Gln Thr Phe Lys Met Asp Ile Ala Glu Arg Arg Glu Pro Ala
1045 1050 1055
Met Cys Ser Gln Gln Asn Pro Asn Ala Arg Phe Pro Leu Cys Ser Ser
1060 1065 1070
Leu Ala Pro Leu Pro Leu
1075

<210> 45
<211> 2103
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2103)
<223> MOOSE03412

<400> 45

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atg gtt ggc aaa ctt tcc aga agg atc tac ttg agt tct gca aga atg   48
Met Val Gly Lys Leu Ser Arg Arg Ile Tyr Leu Ser Ser Ala Arg Met
 1               5                  10                  15

gtt act aca gta ccc cat gtg ttt tca aaa ctg tta gaa atg ctg agt   96
Val Thr Thr Val Pro His Val Phe Ser Lys Leu Leu Glu Met Leu Ser
            20                  25                  30

gtt tcc agt tcc act cac ttc acc agg atg cgt cgc cgt ttg atg gct   144
Val Ser Ser Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala
        35                  40                  45

att gca gat gag gtg gaa att gcc gaa gcc atc cag ttg ggc gta gaa   192
Ile Ala Asp Glu Val Glu Ile Ala Glu Ala Ile Gln Leu Gly Val Glu
    50                  55                  60

gac act ttg gat ggt caa cag gac agc ttc ttg cag gca tct gtt ccc   240
Asp Thr Leu Asp Gly Gln Gln Asp Ser Phe Leu Gln Ala Ser Val Pro
65                  70                  75                  80

aac aac tat ctg gaa acc aca gag aac agt tcc cct gag tgc aca atc   288
Asn Asn Tyr Leu Glu Thr Thr Glu Asn Ser Ser Pro Glu Cys Thr Ile
                85                  90                  95

cat tta gag aaa act gga aaa gga tta tgt gct aca aaa ttg agt gcc   336
His Leu Glu Lys Thr Gly Lys Gly Leu Cys Ala Thr Lys Leu Ser Ala
            100                 105                 110

agt tca gag gac att tct gag aga ctg gcc agc att tca gta gga cct   384
Ser Ser Glu Asp Ile Ser Glu Arg Leu Ala Ser Ile Ser Val Gly Pro
        115                 120                 125

tct agt tca aca aca aca aca aca aca aca gag caa cca aag cca atg   432
Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr Glu Gln Pro Lys Pro Met
    130                 135                 140

gtt caa aca aaa ggc aga ccc cac agt cag tgt ttg aac tcc tct cct   480
Val Gln Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro
145                 150                 155                 160

tta tct cat cat tcc caa tta atg ttt cca gcc ttg tca acc cct tct   528
Leu Ser His His Ser Gln Leu Met Phe Pro Ala Leu Ser Thr Pro Ser
                165                 170                 175

tct tct acc cca tct gta cca gct ggc act gca aca gat gtc tct aag   576
Ser Ser Thr Pro Ser Val Pro Ala Gly Thr Ala Thr Asp Val Ser Lys
            180                 185                 190

cat aga ctt cag gga ttc att ccc tgc aga ata cct tct gca tct cct   624
His Arg Leu Gln Gly Phe Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro
        195                 200                 205

caa aca cag cgc aag ttt tct cta caa ttc cac aga aac tgt cct gaa   672
Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe His Arg Asn Cys Pro Glu
    210                 215                 220

aac aaa gac tca gat aaa ctt tcc cca gtc ttt act cag tca aga ccc   720
Asn Lys Asp Ser Asp Lys Leu Ser Pro Val Phe Thr Gln Ser Arg Pro
225                 230                 235                 240
```

```
ttg ccc tcc agt aac ata cac agg cca aag cca tct cga cct acc cca   768
Leu Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg Pro Thr Pro
                245                 250                 255

ggt aat aca agt aaa cag gga gat ccc tca aaa aat agc atg aca ctt   816
Gly Asn Thr Ser Lys Gln Gly Asp Pro Ser Lys Asn Ser Met Thr Leu
            260                 265                 270

gat ctg aac agt agt tcc aaa tgt gat gac agc ttt ggc tgt agc agc   864
Asp Leu Asn Ser Ser Ser Lys Cys Asp Asp Ser Phe Gly Cys Ser Ser
        275                 280                 285

aat agt agt aat gct gtt ata ccc agt gac gag aca gtg ttc acc cca   912
Asn Ser Ser Asn Ala Val Ile Pro Ser Asp Glu Thr Val Phe Thr Pro
    290                 295                 300

gta gag gag aaa tgc aga tta gat gtc aat aca gag ctc aac tcc agt   960
Val Glu Glu Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser
305                 310                 315                 320

att gag gac ctt ctt gaa gca tct atg cct tca agt gat aca aca gta  1008
Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp Thr Thr Val
                325                 330                 335

act ttt aag tca gaa gtt gct gtc ctg tct cct gaa aag gct gaa aat  1056
Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys Ala Glu Asn
            340                 345                 350

gat gat acc tac aaa gat gat gtg aat cat aat caa aag tgc aaa gag  1104
Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu
        355                 360                 365

aag atg gaa gct gaa gaa gaa gaa gct tta gca att gcc atg gca atg  1152
Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala Met Ala Met
    370                 375                 380

tca gcg tct cag gat gcc ctc ccc ata gtt cct cag ctg cag gtt gaa  1200
Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu Gln Val Glu
385                 390                 395                 400

aat gga gaa gat atc atc att att caa cag gat aca cca gag act cta  1248
Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu
                405                 410                 415

cca gga cat acc aaa gca aaa caa ccg tat aga gaa gac act gaa tgg  1296
Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp
            420                 425                 430

ctg aaa ggt caa cag ata ggc ctt gga gca ttt tct tct tgt tat cag  1344
Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln
        435                 440                 445

gct caa gat gtg gga act gga act tta atg gct gtt aaa cag gtg act  1392
Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys Gln Val Thr
    450                 455                 460

tat gtc aga aac aca tct tct gag caa gaa gaa gta gta gaa gca cta  1440
Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val Glu Ala Leu
465                 470                 475                 480
```

```
aga gaa gag ata aga atg atg agc cat ctg aat cat cca aac atc att   1488
Arg Glu Glu Ile Arg Met Met Ser His Leu Asn His Pro Asn Ile Ile
                485                 490                 495

agg atg ttg gga gcc acg tgt gag aag agc aat tac aat ctc ttc att   1536
Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile
            500                 505                 510

gaa tgg atg gca ggg gga tcg gtg gct cat ttg ctg agt aaa tat gga   1584
Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly
        515                 520                 525

gcc ttc aaa gaa tca gta gtt att aac tac act gaa cag tta ctc cgt   1632
Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg
    530                 535                 540

ggc ctt tcg tat ctc cat gaa aac caa atc att cac aga gat gtc aaa   1680
Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys
545                 550                 555                 560

ggt gcc aat ttg cta att gac agc act ggt cag aga cta aga att gca   1728
Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala
                565                 570                 575

gat ttt gga gct gca gcc agg ttg gca tca aaa gga act ggt gca gga   1776
Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly
            580                 585                 590

gag ttt cag gga caa tta ctg ggg aca att gca ttt atg gca cct gag   1824
Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu
        595                 600                 605

gta cta aga ggt caa cag tat gga agg agc tgt gat gta tgg agt gtt   1872
Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val
    610                 615                 620

ggc tgt gct att ata gaa atg gct tgt gca aaa cca cca tgg aat gca   1920
Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala
625                 630                 635                 640

gaa aaa cac tcc aat cat ctt gct ttg ata ttt aag att gct agt gca   1968
Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala
                645                 650                 655

act act gct cca tcg atc cct tca cat ttg tct cct ggt tta cga gat   2016
Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp
            660                 665                 670

gtg gct ctt cgt tgt tta gaa ctt caa cct cag gac aga cct cca tca   2064
Val Ala Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser
        675                 680                 685

aga gag cta ctg aag cat cca gtc ttt cgt act aca tgg               2103
Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp
    690                 695                 700
```

<210> 46
<211> 701
<212> PRT
<213> Homo sapiens

<400> 46

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Met Val Gly Lys Leu Ser Arg Arg Ile Tyr Leu Ser Ser Ala Arg Met
 1               5                  10                  15
Val Thr Thr Val Pro His Val Phe Ser Lys Leu Leu Glu Met Leu Ser
            20                  25                  30
Val Ser Ser Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala
        35                  40                  45
Ile Ala Asp Glu Val Glu Ile Ala Glu Ala Ile Gln Leu Gly Val Glu
    50                  55                  60
Asp Thr Leu Asp Gly Gln Gln Asp Ser Phe Leu Gln Ala Ser Val Pro
65                  70                  75                  80
Asn Asn Tyr Leu Glu Thr Thr Glu Asn Ser Ser Pro Glu Cys Thr Ile
                85                  90                  95
His Leu Glu Lys Thr Gly Lys Gly Leu Cys Ala Thr Lys Leu Ser Ala
            100                 105                 110
Ser Ser Glu Asp Ile Ser Glu Arg Leu Ala Ser Ile Ser Val Gly Pro
        115                 120                 125
Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr Glu Gln Pro Lys Pro Met
    130                 135                 140
Val Gln Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro
145                 150                 155                 160
Leu Ser His His Ser Gln Leu Met Phe Pro Ala Leu Ser Thr Pro Ser
                165                 170                 175
Ser Ser Thr Pro Ser Val Pro Ala Gly Thr Ala Thr Asp Val Ser Lys
            180                 185                 190
His Arg Leu Gln Gly Phe Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro
        195                 200                 205
Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe His Arg Asn Cys Pro Glu
    210                 215                 220
Asn Lys Asp Ser Asp Lys Leu Ser Pro Val Phe Thr Gln Ser Arg Pro
225                 230                 235                 240
Leu Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg Pro Thr Pro
                245                 250                 255
Gly Asn Thr Ser Lys Gln Gly Asp Pro Ser Lys Asn Ser Met Thr Leu
            260                 265                 270
Asp Leu Asn Ser Ser Ser Lys Cys Asp Asp Ser Phe Gly Cys Ser Ser
        275                 280                 285
Asn Ser Ser Asn Ala Val Ile Pro Ser Asp Glu Thr Val Phe Thr Pro
    290                 295                 300
Val Glu Glu Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser
305                 310                 315                 320
Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp Thr Thr Val
                325                 330                 335
Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys Ala Glu Asn
            340                 345                 350
Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu
        355                 360                 365
Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala Met Ala Met
    370                 375                 380
Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu Gln Val Glu
385                 390                 395                 400
Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu
                405                 410                 415
Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp
            420                 425                 430
Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln
        435                 440                 445
Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys Gln Val Thr
    450                 455                 460
Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val Glu Ala Leu
465                 470                 475                 480
```

```
Arg Glu Glu Ile Arg Met Met Ser His Leu Asn His Pro Asn Ile Ile
                485                 490                 495
Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile
            500                 505                 510
Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly
        515                 520                 525
Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg
    530                 535                 540
Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys
545                 550                 555                 560
Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala
                565                 570                 575
Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly
            580                 585                 590
Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu
        595                 600                 605
Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val
    610                 615                 620
Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala
625                 630                 635                 640
Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala
                645                 650                 655
Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp
            660                 665                 670
Val Ala Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser
        675                 680                 685
Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp
    690                 695                 700
```

<210> 47
<211> 1794
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1794)
<223> MOOSE03452

<400> 47

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atg gaa aag tac cac gtg ttg gag atg att gga gaa ggc tct ttt ggg   48
Met Glu Lys Tyr His Val Leu Glu Met Ile Gly Glu Gly Ser Phe Gly
 1               5                  10                  15

agg gtg tac aag ggt cga aga aaa tac agt gct cag gtc gtg gcc ctg   96
Arg Val Tyr Lys Gly Arg Arg Lys Tyr Ser Ala Gln Val Val Ala Leu
            20                  25                  30

aag ttc atc cca aaa ttg ggg cgc tca gag aag gag ctg agg aat ttg   144
Lys Phe Ile Pro Lys Leu Gly Arg Ser Glu Lys Glu Leu Arg Asn Leu
        35                  40                  45

caa cga gag att gaa ata atg cgg ggt ctg cgg cat ccc aac att gtg   192
Gln Arg Glu Ile Glu Ile Met Arg Gly Leu Arg His Pro Asn Ile Val
    50                  55                  60

cat atg ctt gac agc ttt gaa act gat aaa gag gtg gtg gtg gtg aca   240
His Met Leu Asp Ser Phe Glu Thr Asp Lys Glu Val Val Val Val Thr
65                  70                  75                  80
```

```
gac tat gct gag gga gag ctc ttt cag atc cta gaa gat gac gga aaa   288
Asp Tyr Ala Glu Gly Glu Leu Phe Gln Ile Leu Glu Asp Asp Gly Lys
                 85                  90                  95

ctt cct gaa gac cag gtt cag gcc att gct gcc cag ttg gtg tca gcc   336
Leu Pro Glu Asp Gln Val Gln Ala Ile Ala Ala Gln Leu Val Ser Ala
            100                 105                 110

ctg tac tat ctg cat tcc cac cgc atc cta cac cga gat atg aag cct   384
Leu Tyr Tyr Leu His Ser His Arg Ile Leu His Arg Asp Met Lys Pro
        115                 120                 125

cag aac atc ctc ctc gcc aag ggt ggt ggc atc aag ctc tgt gac ttt   432
Gln Asn Ile Leu Leu Ala Lys Gly Gly Gly Ile Lys Leu Cys Asp Phe
    130                 135                 140

gga ttt gcc cgg gct atg agc acc aat aca atg gtg ctg aca tcc atc   480
Gly Phe Ala Arg Ala Met Ser Thr Asn Thr Met Val Leu Thr Ser Ile
145                 150                 155                 160

aaa ggc aca cca ctc tat atg tct cca gag ctg gtg gag gag cga cca   528
Lys Gly Thr Pro Leu Tyr Met Ser Pro Glu Leu Val Glu Glu Arg Pro
                165                 170                 175

tac gac cac aca gcg gac ctc tgg tct gtt ggc tgc ata cta tat gaa   576
Tyr Asp His Thr Ala Asp Leu Trp Ser Val Gly Cys Ile Leu Tyr Glu
            180                 185                 190

ctg gca gta ggc acc cct ccc ttc tat gct aca agc atc ttt cag ctg   624
Leu Ala Val Gly Thr Pro Pro Phe Tyr Ala Thr Ser Ile Phe Gln Leu
        195                 200                 205

gtc agc ctc att ctc aag gac cct gtg cgc tgg ccc tca acc atc agt   672
Val Ser Leu Ile Leu Lys Asp Pro Val Arg Trp Pro Ser Thr Ile Ser
    210                 215                 220

ccc tgc ttt aag aac ttc ctg cag gga ctg ctc acc aaa gac cca cgg   720
Pro Cys Phe Lys Asn Phe Leu Gln Gly Leu Leu Thr Lys Asp Pro Arg
225                 230                 235                 240

cag cga ctg tcc tgg cca gac ctc tta tat cac ccc ttt att gct ggt   768
Gln Arg Leu Ser Trp Pro Asp Leu Leu Tyr His Pro Phe Ile Ala Gly
                245                 250                 255

cat gtc acc ata ata act gag cca gca ggc cca gat ttg ggg acc cca   816
His Val Thr Ile Ile Thr Glu Pro Ala Gly Pro Asp Leu Gly Thr Pro
            260                 265                 270

ttc acc agc cgc cta ccc cca gaa ctt cag gtc cta aag gac gaa cag   864
Phe Thr Ser Arg Leu Pro Pro Glu Leu Gln Val Leu Lys Asp Glu Gln
        275                 280                 285

gcc cat cgg ttg gcc ccc aag ggt aat cag tct cgc atc ttg act cag   912
Ala His Arg Leu Ala Pro Lys Gly Asn Gln Ser Arg Ile Leu Thr Gln
    290                 295                 300

gcc tat aaa cgc atg gct gag gag gcc atg cag aag gtt gca gtg agc   960
Ala Tyr Lys Arg Met Ala Glu Glu Ala Met Gln Lys Val Ala Val Ser
305                 310                 315                 320
```

caa gat tac gcc act gaa ctc cag cct ggt gac aga gca aga ctc cgt 1008
Gln Asp Tyr Ala Thr Glu Leu Gln Pro Gly Asp Arg Ala Arg Leu Arg
325 330 335

ctc aaa aaa aaa aaa aaa aaa aag caa tta aac tta tac cta aac ttt 1056
Leu Lys Lys Lys Lys Lys Lys Gln Leu Asn Leu Tyr Leu Asn Phe
340 345 350

tta gac tat cta gca cat aaa gca ata atg gat tct gaa gtt aag gct 1104
Leu Asp Tyr Leu Ala His Lys Ala Ile Met Asp Ser Glu Val Lys Ala
355 360 365

tca tct aga tac aga ttt tca gca aat gac aac ttc cta ttc aca cat 1152
Ser Ser Arg Tyr Arg Phe Ser Ala Asn Asp Asn Phe Leu Phe Thr His
370 375 380

tca ttt ctg cat ttg gtt atg ctg ggg gcg ggc gga tcg ctt gag cag 1200
Ser Phe Leu His Leu Val Met Leu Gly Ala Gly Gly Ser Leu Glu Gln
385 390 395 400

gag ttc aag ttc gca gtg agc tat gat cac gtc gct gca ctc cag cct 1248
Glu Phe Lys Phe Ala Val Ser Tyr Asp His Val Ala Ala Leu Gln Pro
405 410 415

ggg cga cag agc gag att ctg tct cta aaa aag aaa aca gtc cat agg 1296
Gly Arg Gln Ser Glu Ile Leu Ser Leu Lys Lys Lys Thr Val His Arg
420 425 430

gat aga aag aga gag tcc tgg atg ctc cga atg gag cct ttc aga gct 1344
Asp Arg Lys Arg Glu Ser Trp Met Leu Arg Met Glu Pro Phe Arg Ala
435 440 445

tta acc acg gga cta cat ctc cca gaa ttc cgc tcg ccg gat ccc acc 1392
Leu Thr Thr Gly Leu His Leu Pro Glu Phe Arg Ser Pro Asp Pro Thr
450 455 460

gca ctg aag gga ctg cgc gtg cgc gag tca ggt gac gac ccg ccc cta 1440
Ala Leu Lys Gly Leu Arg Val Arg Glu Ser Gly Asp Asp Pro Pro Leu
465 470 475 480

cag gcc cca gaa ccc ccg aga ttc ccc gcg ctt gcc tcc cgc cct ctt 1488
Gln Ala Pro Glu Pro Pro Arg Phe Pro Ala Leu Ala Ser Arg Pro Leu
485 490 495

ctt cca gac tct cgg tct aaa agc cta aaa aag aaa ata aaa att aca 1536
Leu Pro Asp Ser Arg Ser Lys Ser Leu Lys Lys Lys Ile Lys Ile Thr
500 505 510

tat aat tta cca ccg ttg tta att ttg gta ggt act ttt cca gtc gag 1584
Tyr Asn Leu Pro Pro Leu Leu Ile Leu Val Gly Thr Phe Pro Val Glu
515 520 525

tgt gtg cat gtg aaa tca gct gtt gaa ata gtt ttg agt gag cca cca 1632
Cys Val His Val Lys Ser Ala Val Glu Ile Val Leu Ser Glu Pro Pro
530 535 540

cac cag gtc tgt ttt tgt gtt ttc ttt tct ttt gag atg gag tct tgc 1680
His Gln Val Cys Phe Cys Val Phe Phe Ser Phe Glu Met Glu Ser Cys
545 550 555 560

```
tct gta cct cag ctg gaa tta cag aaa tca ccc gtc ttc tgc gtt gat   1728
Ser Val Pro Gln Leu Glu Leu Gln Lys Ser Pro Val Phe Cys Val Asp
                565                 570                 575

cac gtt ggg agc agc aga tca gag ctg ttc cta ttc ggc cat ctt tct   1776
His Val Gly Ser Ser Arg Ser Glu Leu Phe Leu Phe Gly His Leu Ser
            580                 585                 590

ttt ctt tct ttt ctt tcc                                           1794
Phe Leu Ser Phe Leu Ser
        595
```

<210> 48
<211> 598
<212> PRT
<213> Homo sapiens

<400> 48

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Met Glu Lys Tyr His Val Leu Glu Met Ile Gly Glu Gly Ser Phe Gly
 1               5                  10                  15
Arg Val Tyr Lys Gly Arg Arg Lys Tyr Ser Ala Gln Val Val Ala Leu
            20                  25                  30
Lys Phe Ile Pro Lys Leu Gly Arg Ser Glu Lys Glu Leu Arg Asn Leu
        35                  40                  45
Gln Arg Glu Ile Glu Ile Met Arg Gly Leu Arg His Pro Asn Ile Val
    50                  55                  60
His Met Leu Asp Ser Phe Glu Thr Asp Lys Glu Val Val Val Val Thr
65                  70                  75                  80
Asp Tyr Ala Glu Gly Glu Leu Phe Gln Ile Leu Glu Asp Asp Gly Lys
                85                  90                  95
Leu Pro Glu Asp Gln Val Gln Ala Ile Ala Ala Gln Leu Val Ser Ala
            100                 105                 110
Leu Tyr Tyr Leu His Ser His Arg Ile Leu His Arg Asp Met Lys Pro
        115                 120                 125
Gln Asn Ile Leu Leu Ala Lys Gly Gly Gly Ile Lys Leu Cys Asp Phe
    130                 135                 140
Gly Phe Ala Arg Ala Met Ser Thr Asn Thr Met Val Leu Thr Ser Ile
145                 150                 155                 160
Lys Gly Thr Pro Leu Tyr Met Ser Pro Glu Leu Val Glu Glu Arg Pro
                165                 170                 175
Tyr Asp His Thr Ala Asp Leu Trp Ser Val Gly Cys Ile Leu Tyr Glu
            180                 185                 190
Leu Ala Val Gly Thr Pro Pro Phe Tyr Ala Thr Ser Ile Phe Gln Leu
        195                 200                 205
Val Ser Leu Ile Leu Lys Asp Pro Val Arg Trp Pro Ser Thr Ile Ser
    210                 215                 220
Pro Cys Phe Lys Asn Phe Leu Gln Gly Leu Leu Thr Lys Asp Pro Arg
225                 230                 235                 240
Gln Arg Leu Ser Trp Pro Asp Leu Leu Tyr His Pro Phe Ile Ala Gly
                245                 250                 255
His Val Thr Ile Ile Thr Glu Pro Ala Gly Pro Asp Leu Gly Thr Pro
            260                 265                 270
Phe Thr Ser Arg Leu Pro Pro Glu Leu Gln Val Leu Lys Asp Glu Gln
        275                 280                 285
Ala His Arg Leu Ala Pro Lys Gly Asn Gln Ser Arg Ile Leu Thr Gln
    290                 295                 300
Ala Tyr Lys Arg Met Ala Glu Glu Ala Met Gln Lys Val Ala Val Ser
305                 310                 315                 320
Gln Asp Tyr Ala Thr Glu Leu Gln Pro Gly Asp Arg Ala Arg Leu Arg
                325                 330                 335
```

```
Leu Lys Lys Lys Lys Lys Lys Gln Leu Asn Leu Tyr Leu Asn Phe
            340                 345                 350
Leu Asp Tyr Leu Ala His Lys Ala Ile Met Asp Ser Glu Val Lys Ala
        355                 360                 365
Ser Ser Arg Tyr Arg Phe Ser Ala Asn Asp Asn Phe Leu Phe Thr His
    370                 375                 380
Ser Phe Leu His Leu Val Met Leu Gly Ala Gly Gly Ser Leu Glu Gln
385                 390                 395                 400
Glu Phe Lys Phe Ala Val Ser Tyr Asp His Val Ala Ala Leu Gln Pro
                405                 410                 415
Gly Arg Gln Ser Glu Ile Leu Ser Leu Lys Lys Lys Thr Val His Arg
            420                 425                 430
Asp Arg Lys Arg Glu Ser Trp Met Leu Arg Met Glu Pro Phe Arg Ala
        435                 440                 445
Leu Thr Thr Gly Leu His Leu Pro Glu Phe Arg Ser Pro Asp Pro Thr
    450                 455                 460
Ala Leu Lys Gly Leu Arg Val Arg Glu Ser Gly Asp Asp Pro Pro Leu
465                 470                 475                 480
Gln Ala Pro Glu Pro Pro Arg Phe Pro Ala Leu Ala Ser Arg Pro Leu
                485                 490                 495
Leu Pro Asp Ser Arg Ser Lys Ser Leu Lys Lys Lys Ile Lys Ile Thr
            500                 505                 510
Tyr Asn Leu Pro Pro Leu Leu Ile Leu Val Gly Thr Phe Pro Val Glu
        515                 520                 525
Cys Val His Val Lys Ser Ala Val Glu Ile Val Leu Ser Glu Pro Pro
    530                 535                 540
His Gln Val Cys Phe Cys Val Phe Phe Ser Phe Glu Met Glu Ser Cys
545                 550                 555                 560
Ser Val Pro Gln Leu Glu Leu Gln Lys Ser Pro Val Phe Cys Val Asp
                565                 570                 575
His Val Gly Ser Ser Arg Ser Glu Leu Phe Leu Phe Gly His Leu Ser
            580                 585                 590
Phe Leu Ser Phe Leu Ser
        595
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<210> 49
<211> 1638
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1638)
<223> MOOSE03453

<400> 49

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atg gat gac tac atg gtc ctg aga atg att ggg gag ggc tcc ttc ggc   48
Met Asp Asp Tyr Met Val Leu Arg Met Ile Gly Glu Gly Ser Phe Gly
 1               5                  10                  15

aga gct ctt ttg gtt cag cat gaa agc agt aat cag atg ttt gcc atg   96
Arg Ala Leu Leu Val Gln His Glu Ser Ser Asn Gln Met Phe Ala Met
             20                  25                  30

aaa gaa ata agg ctt ccc aag tct ttc tct aat aca cag aat tct agg   144
Lys Glu Ile Arg Leu Pro Lys Ser Phe Ser Asn Thr Gln Asn Ser Arg
         35                  40                  45

aag gag gct gtt ctt tta gcc aaa atg aaa cac cct aat att gtt gcc   192
Lys Glu Ala Val Leu Leu Ala Lys Met Lys His Pro Asn Ile Val Ala
     50                  55                  60
```

```
ttc aaa gaa tca ttt gaa gct gaa gga cac ttg tat att gtg atg gaa   240
Phe Lys Glu Ser Phe Glu Ala Glu Gly His Leu Tyr Ile Val Met Glu
 65                  70                  75                  80

tac tgt gat gga ggg gat cta atg caa aag att aaa cag cag aaa gga   288
Tyr Cys Asp Gly Gly Asp Leu Met Gln Lys Ile Lys Gln Gln Lys Gly
                85                  90                  95

aag tta ttt cct gaa gac atg ata ctt aat tgg ttt acc caa atg tgc   336
Lys Leu Phe Pro Glu Asp Met Ile Leu Asn Trp Phe Thr Gln Met Cys
            100                 105                 110

ctt gga gta aat cac att cac aag aaa cgt gtg cta cac aga gat atc   384
Leu Gly Val Asn His Ile His Lys Lys Arg Val Leu His Arg Asp Ile
        115                 120                 125

aag tcc aag aat atc ttc ctc act cag aat gga aaa gtg aaa ttg gga   432
Lys Ser Lys Asn Ile Phe Leu Thr Gln Asn Gly Lys Val Lys Leu Gly
    130                 135                 140

gac ttt gga tct gcc cgt ctt ctc tcc aat ccg atg gca ttt gct tgt   480
Asp Phe Gly Ser Ala Arg Leu Leu Ser Asn Pro Met Ala Phe Ala Cys
145                 150                 155                 160

acc tat gtg gga act cct tat tat gtg cct cca gaa att tgg gaa aac   528
Thr Tyr Val Gly Thr Pro Tyr Tyr Val Pro Pro Glu Ile Trp Glu Asn
                165                 170                 175

ctg cct tat aac aat aaa agt gac atc tgg tcc ttg ggt tgc atc ctg   576
Leu Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ser Leu Gly Cys Ile Leu
            180                 185                 190

tat gaa ctc tgt acc ctt aag cat cca ttt cag gca aat agt tgg aaa   624
Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Gln Ala Asn Ser Trp Lys
        195                 200                 205

aat ctt atc ctc aaa gta tgt caa ggg tgc atc agt cca ctg ccg tct   672
Asn Leu Ile Leu Lys Val Cys Gln Gly Cys Ile Ser Pro Leu Pro Ser
    210                 215                 220

cat tac tcc tat gaa ctt cag ttc cta gtc aag cag atg ttt aaa agg   720
His Tyr Ser Tyr Glu Leu Gln Phe Leu Val Lys Gln Met Phe Lys Arg
225                 230                 235                 240

aat ccc tca cat cgc ccc tcg gct aca acg ctt ctc tct cga ggc atc   768
Asn Pro Ser His Arg Pro Ser Ala Thr Thr Leu Leu Ser Arg Gly Ile
                245                 250                 255

gta gct cgg ctt gtc cag aag tgc tta ccc ccc gag gca atc tgc ctg   816
Val Ala Arg Leu Val Gln Lys Cys Leu Pro Pro Glu Ala Ile Cys Leu
            260                 265                 270

tct cgg ctt ccc aaa gcg gga gga tcg cct gag cct ggg aag ttg agg   864
Ser Arg Leu Pro Lys Ala Gly Gly Ser Pro Glu Pro Gly Lys Leu Arg
        275                 280                 285

agg gca gtg agc tat gat cgc acc tct gca ctc cag cct ggg caa cac   912
Arg Ala Val Ser Tyr Asp Arg Thr Ser Ala Leu Gln Pro Gly Gln His
    290                 295                 300
```

```
agc aag act ctg tct caa aaa gaa aag aat ttc cat ccc cta aaa tgt   960
Ser Lys Thr Leu Ser Gln Lys Glu Lys Asn Phe His Pro Leu Lys Cys
305                 310                 315                 320

ttc ctt caa gag gaa gaa caa gat aga aag ggt agc cat act gat ttg   1008
Phe Leu Gln Glu Glu Glu Gln Asp Arg Lys Gly Ser His Thr Asp Leu
                325                 330                 335

gaa agc att aat gaa aat tta gtt gaa agt gca ttg aga aga gta aac   1056
Glu Ser Ile Asn Glu Asn Leu Val Glu Ser Ala Leu Arg Arg Val Asn
            340                 345                 350

aga gaa gaa aaa ggt aat cag ggg ctg gaa gtc agg gta gaa atg aca   1104
Arg Glu Glu Lys Gly Asn Gln Gly Leu Glu Val Arg Val Glu Met Thr
        355                 360                 365

agt cag caa agc atc aag agt gag gaa gaa aaa ctc cgg cgg cag caa   1152
Ser Gln Gln Ser Ile Lys Ser Glu Glu Glu Lys Leu Arg Arg Gln Gln
    370                 375                 380

cag cga cta cga ggg atg gcg gcg gct gca gca gga act gca aca tcc   1200
Gln Arg Leu Arg Gly Met Ala Ala Ala Ala Ala Gly Thr Ala Thr Ser
385                 390                 395                 400

cag agg tgc ata ctg ggg aaa agg ctg aaa aaa gtc tgc aag aag aaa   1248
Gln Arg Cys Ile Leu Gly Lys Arg Leu Lys Lys Val Cys Lys Lys Lys
                405                 410                 415

aat caa tac ttt tca ttg agt gat tac tgg atg tca cat aca gat cta   1296
Asn Gln Tyr Phe Ser Leu Ser Asp Tyr Trp Met Ser His Thr Asp Leu
            420                 425                 430

ggc aag ccc aac acc ctg gat agc tgg gac tac agg cga cca cca cca   1344
Gly Lys Pro Asn Thr Leu Asp Ser Trp Asp Tyr Arg Arg Pro Pro Pro
        435                 440                 445

cgc ccg gcc aat ttt ttt gta ttt tta gta gag atg ggg ttt cac cat   1392
Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His His
    450                 455                 460

gtt agc cag gat ggt ctg ggt gat aag gct tat tct caa act tgc tta   1440
Val Ser Gln Asp Gly Leu Gly Asp Lys Ala Tyr Ser Gln Thr Cys Leu
465                 470                 475                 480

tcc cag ttt tgg tat gtg aat agt agg cct att cag tca gca aac agg   1488
Ser Gln Phe Trp Tyr Val Asn Ser Arg Pro Ile Gln Ser Ala Asn Arg
                485                 490                 495

aca tct gca ctc tta gca aat tct aga aat tca tgt caa gga tac cag   1536
Thr Ser Ala Leu Leu Ala Asn Ser Arg Asn Ser Cys Gln Gly Tyr Gln
            500                 505                 510

atg gaa aaa aaa gat cac tac gtt gca ctc cag cct ggg caa cag agt   1584
Met Glu Lys Lys Asp His Tyr Val Ala Leu Gln Pro Gly Gln Gln Ser
        515                 520                 525

gag act ctg tct caa aaa aaa aaa aaa aaa gat tat gtg tgg cta gag   1632
Glu Thr Leu Ser Gln Lys Lys Lys Lys Lys Asp Tyr Val Trp Leu Glu
    530                 535                 540
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ttg agg 1638
Leu Arg
545

<210> 50
<211> 546
<212> PRT
<213> Homo sapiens

<400> 50
Met Asp Asp Tyr Met Val Leu Arg Met Ile Gly Glu Gly Ser Phe Gly
1 5 10 15
Arg Ala Leu Leu Val Gln His Glu Ser Ser Asn Gln Met Phe Ala Met
20 25 30
Lys Glu Ile Arg Leu Pro Lys Ser Phe Ser Asn Thr Gln Asn Ser Arg
35 40 45
Lys Glu Ala Val Leu Leu Ala Lys Met Lys His Pro Asn Ile Val Ala
50 55 60
Phe Lys Glu Ser Phe Glu Ala Glu Gly His Leu Tyr Ile Val Met Glu
65 70 75 80
Tyr Cys Asp Gly Gly Asp Leu Met Gln Lys Ile Lys Gln Gln Lys Gly
85 90 95
Lys Leu Phe Pro Glu Asp Met Ile Leu Asn Trp Phe Thr Gln Met Cys
100 105 110
Leu Gly Val Asn His Ile His Lys Lys Arg Val Leu His Arg Asp Ile
115 120 125
Lys Ser Lys Asn Ile Phe Leu Thr Gln Asn Gly Lys Val Lys Leu Gly
130 135 140
Asp Phe Gly Ser Ala Arg Leu Leu Ser Asn Pro Met Ala Phe Ala Cys
145 150 155 160
Thr Tyr Val Gly Thr Pro Tyr Tyr Val Pro Pro Glu Ile Trp Glu Asn
165 170 175
Leu Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ser Leu Gly Cys Ile Leu
180 185 190
Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Gln Ala Asn Ser Trp Lys
195 200 205
Asn Leu Ile Leu Lys Val Cys Gln Gly Cys Ile Ser Pro Leu Pro Ser
210 215 220
His Tyr Ser Tyr Glu Leu Gln Phe Leu Val Lys Gln Met Phe Lys Arg
225 230 235 240
Asn Pro Ser His Arg Pro Ser Ala Thr Thr Leu Leu Ser Arg Gly Ile
245 250 255
Val Ala Arg Leu Val Gln Lys Cys Leu Pro Pro Glu Ala Ile Cys Leu
260 265 270
Ser Arg Leu Pro Lys Ala Gly Gly Ser Pro Glu Pro Gly Lys Leu Arg
275 280 285
Arg Ala Val Ser Tyr Asp Arg Thr Ser Ala Leu Gln Pro Gly Gln His
290 295 300
Ser Lys Thr Leu Ser Gln Lys Glu Lys Asn Phe His Pro Leu Lys Cys
305 310 315 320
Phe Leu Gln Glu Glu Glu Gln Asp Arg Lys Gly Ser His Thr Asp Leu
325 330 335
Glu Ser Ile Asn Glu Asn Leu Val Glu Ser Ala Leu Arg Arg Val Asn
340 345 350
Arg Glu Glu Lys Gly Asn Gln Gly Leu Glu Val Arg Val Glu Met Thr
355 360 365
Ser Gln Gln Ser Ile Lys Ser Glu Glu Glu Lys Leu Arg Arg Gln Gln
370 375 380
Gln Arg Leu Arg Gly Met Ala Ala Ala Ala Ala Gly Thr Ala Thr Ser
385 390 395 400

```
Gln Arg Cys Ile Leu Gly Lys Arg Leu Lys Lys Val Cys Lys Lys Lys
                405                 410                 415
Asn Gln Tyr Phe Ser Leu Ser Asp Tyr Trp Met Ser His Thr Asp Leu
            420                 425                 430
Gly Lys Pro Asn Thr Leu Asp Ser Trp Asp Tyr Arg Arg Pro Pro Pro
        435                 440                 445
Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His His
    450                 455                 460
Val Ser Gln Asp Gly Leu Gly Asp Lys Ala Tyr Ser Gln Thr Cys Leu
465                 470                 475                 480
Ser Gln Phe Trp Tyr Val Asn Ser Arg Pro Ile Gln Ser Ala Asn Arg
                485                 490                 495
Thr Ser Ala Leu Leu Ala Asn Ser Arg Asn Ser Cys Gln Gly Tyr Gln
            500                 505                 510
Met Glu Lys Lys Asp His Tyr Val Ala Leu Gln Pro Gly Gln Gln Ser
        515                 520                 525
Glu Thr Leu Ser Gln Lys Lys Lys Lys Lys Asp Tyr Val Trp Leu Glu
    530                 535                 540
Leu Arg
545
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<210> 51
<211> 1632
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1632)
<223> MOOSE03455

<400> 51

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tac agg aat gtt tct cgg gct cat gaa agg ttg cac agc tgc tta gtt   48
Tyr Arg Asn Val Ser Arg Ala His Glu Arg Leu His Ser Cys Leu Val
 1               5                  10                  15

ggc ctg gga gtg ttt ctg cgg ggg gtg gcc tac agg gct aag agg gag   96
Gly Leu Gly Val Phe Leu Arg Gly Val Ala Tyr Arg Ala Lys Arg Glu
            20                  25                  30

aga gat ggg gaa tgg cta ctc agt gga gca gtc aaa aaa cac atg gca   144
Arg Asp Gly Glu Trp Leu Leu Ser Gly Ala Val Lys Lys His Met Ala
        35                  40                  45

ttg att aag aac atg gct gat aaa tat ctg aaa tcc ttc cag cac caa   192
Leu Ile Lys Asn Met Ala Asp Lys Tyr Leu Lys Ser Phe Gln His Gln
    50                  55                  60

atg att cct ttt ctt aca gag aat ggc agg ctg ttt att gta atg gaa   240
Met Ile Pro Phe Leu Thr Glu Asn Gly Arg Leu Phe Ile Val Met Glu
65                  70                  75                  80

tat tgt gat gga ggg gat ctc atg aaa agg atc aat aga caa cgg ggt   288
Tyr Cys Asp Gly Gly Asp Leu Met Lys Arg Ile Asn Arg Gln Arg Gly
                85                  90                  95

gtg tta ttt agt gaa gat cag atc ctc ggt tgg ttt gta cag att tct   336
Val Leu Phe Ser Glu Asp Gln Ile Leu Gly Trp Phe Val Gln Ile Ser
            100                 105                 110
```

```
cta gga cta aaa cat att cat gac agg aag ata tta cac agg gac ata   384
Leu Gly Leu Lys His Ile His Asp Arg Lys Ile Leu His Arg Asp Ile
        115                 120                 125

aaa gct cag aac att ttt ctt agc aag aac gga atg gtg gca aag ctt   432
Lys Ala Gln Asn Ile Phe Leu Ser Lys Asn Gly Met Val Ala Lys Leu
    130                 135                 140

ggg gac ttt ggt ata gca aga gtc ctg aat aat tcc atg gaa ctt gct   480
Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Asn Ser Met Glu Leu Ala
145                 150                 155                 160

cga act tgt att gga aca cct tac tac ctg tcc cca gag atc tgt cag   528
Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Gln
                165                 170                 175

aat aaa ccc tac aac aat aaa acg gat att tgg tct ctt ggc tgt gtc   576
Asn Lys Pro Tyr Asn Asn Lys Thr Asp Ile Trp Ser Leu Gly Cys Val
            180                 185                 190

tta tat gag ctc tgc aca ctt aaa cat cct ttt gag ggt aac aac tta   624
Leu Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Glu Gly Asn Asn Leu
        195                 200                 205

cag cag ctg gtt ctg aag att tgt caa gca cat ttt gcc cca ata tct   672
Gln Gln Leu Val Leu Lys Ile Cys Gln Ala His Phe Ala Pro Ile Ser
    210                 215                 220

ccg ggg ttt tct cgt gag ctc cat tcc ttg ata tct cag ctc ttt caa   720
Pro Gly Phe Ser Arg Glu Leu His Ser Leu Ile Ser Gln Leu Phe Gln
225                 230                 235                 240

gta tct cct cga gac cga cca tcc ata aat tcc att ttg aaa agg ccc   768
Val Ser Pro Arg Asp Arg Pro Ser Ile Asn Ser Ile Leu Lys Arg Pro
                245                 250                 255

ttt tta gag aat ctt att ccc aaa tat ttg act cct gag gta agt ttt   816
Phe Leu Glu Asn Leu Ile Pro Lys Tyr Leu Thr Pro Glu Val Ser Phe
            260                 265                 270

gag tac ctt cag aga aaa ttt gaa gct caa caa tat aag ttg aaa gtg   864
Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln Tyr Lys Leu Lys Val
        275                 280                 285

gag aag caa ttg gta agt tct aaa ggc tat tta agg caa aat ctg agt   912
Glu Lys Gln Leu Val Ser Ser Lys Gly Tyr Leu Arg Gln Asn Leu Ser
    290                 295                 300

gca gtt gaa ctg att ctt aaa aat ctc tta aag gcg cca cat tgg aaa   960
Ala Val Glu Leu Ile Leu Lys Asn Leu Leu Lys Ala Pro His Trp Lys
305                 310                 315                 320

ttc atc ctt cca tct ccc aag aag gtc tct aga gtt ggc aca gat cac  1008
Phe Ile Leu Pro Ser Pro Lys Lys Val Ser Arg Val Gly Thr Asp His
                325                 330                 335

tgc ttc ttc aga aga gct tca cat gaa ata gcc agc ctg tac gca cag  1056
Cys Phe Phe Arg Arg Ala Ser His Glu Ile Ala Ser Leu Tyr Ala Gln
            340                 345                 350
```

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ttt cac atg gct ggg gag gcc tca caa tca tgg cag aag gca aag gag   1104
Phe His Met Ala Gly Glu Ala Ser Gln Ser Trp Gln Lys Ala Lys Glu
        355                 360                 365

gag caa agt cat gcc tta cat gaa ggc agg caa gag agc ttg tgg gaa   1152
Glu Gln Ser His Ala Leu His Glu Gly Arg Gln Glu Ser Leu Trp Glu
    370                 375                 380

ctc cta ttt aca aaa cca tca gat ctt cta aag gct gca gtg agc cat   1200
Leu Leu Phe Thr Lys Pro Ser Asp Leu Leu Lys Ala Ala Val Ser His
385                 390                 395                 400

gat tgt gcc act gta ccc cag cct ggg ata cag agc aag act cgg tct   1248
Asp Cys Ala Thr Val Pro Gln Pro Gly Ile Gln Ser Lys Thr Arg Ser
                405                 410                 415

caa aaa aat aaa gcg ctc ctc aca tcc cag acg ggg cgg cgg ggc aaa   1296
Gln Lys Asn Lys Ala Leu Leu Thr Ser Gln Thr Gly Arg Arg Gly Lys
            420                 425                 430

ggc gct ccc cac atc tca gac gat ggg cgg ccg ggc aga gac gct cct   1344
Gly Ala Pro His Ile Ser Asp Asp Gly Arg Pro Gly Arg Asp Ala Pro
        435                 440                 445

cac ttc cta gat ggg atg gcg gcg ggg cag aga cgc tcc tca ctt tcc   1392
His Phe Leu Asp Gly Met Ala Ala Gly Gln Arg Arg Ser Ser Leu Ser
    450                 455                 460

aga ctg ggc agc cag gca gag ggg ctc ctc acg tcc cag acg atg ggc   1440
Arg Leu Gly Ser Gln Ala Glu Gly Leu Leu Thr Ser Gln Thr Met Gly
465                 470                 475                 480

ggc cgg gca gag acg ctc ctc act tcc cag acg ggg ctg agg cag gag   1488
Gly Arg Ala Glu Thr Leu Leu Thr Ser Gln Thr Gly Leu Arg Gln Glu
                485                 490                 495

aat tgc ttg aac ctg ggc ggc gga ggt tgc agt gag cca aga tcg agt   1536
Asn Cys Leu Asn Leu Gly Gly Gly Gly Cys Ser Glu Pro Arg Ser Ser
            500                 505                 510

ggt gag aga ggg cat ccc tgt ctt gtg cca gtt ttc aaa ggg aat gct   1584
Gly Glu Arg Gly His Pro Cys Leu Val Pro Val Phe Lys Gly Asn Ala
        515                 520                 525

tcc agt ttt tgc cca ttc aaa aac aaa gat gag gta agg tgg gtc aga   1632
Ser Ser Phe Cys Pro Phe Lys Asn Lys Asp Glu Val Arg Trp Val Arg
    530                 535                 540
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<210> 52
<211> 544
<212> PRT
<213> Homo sapiens

<400> 52

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Tyr Arg Asn Val Ser Arg Ala His Glu Arg Leu His Ser Cys Leu Val
 1               5                  10                  15
Gly Leu Gly Val Phe Leu Arg Gly Val Ala Tyr Arg Ala Lys Arg Glu
            20                  25                  30
Arg Asp Gly Glu Trp Leu Leu Ser Gly Ala Val Lys Lys His Met Ala
        35                  40                  45
```

```
Leu Ile Lys Asn Met Ala Asp Lys Tyr Leu Lys Ser Phe Gln His Gln
    50                  55                  60
Met Ile Pro Phe Leu Thr Glu Asn Gly Arg Leu Phe Ile Val Met Glu
65                  70                  75                  80
Tyr Cys Asp Gly Gly Asp Leu Met Lys Arg Ile Asn Arg Gln Arg Gly
                85                  90                  95
Val Leu Phe Ser Glu Asp Gln Ile Leu Gly Trp Phe Val Gln Ile Ser
            100                 105                 110
Leu Gly Leu Lys His Ile His Asp Arg Lys Ile Leu His Arg Asp Ile
        115                 120                 125
Lys Ala Gln Asn Ile Phe Leu Ser Lys Asn Gly Met Val Ala Lys Leu
    130                 135                 140
Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Asn Ser Met Glu Leu Ala
145                 150                 155                 160
Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Gln
                165                 170                 175
Asn Lys Pro Tyr Asn Asn Lys Thr Asp Ile Trp Ser Leu Gly Cys Val
            180                 185                 190
Leu Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Glu Gly Asn Asn Leu
        195                 200                 205
Gln Gln Leu Val Leu Lys Ile Cys Gln Ala His Phe Ala Pro Ile Ser
    210                 215                 220
Pro Gly Phe Ser Arg Glu Leu His Ser Leu Ile Ser Gln Leu Phe Gln
225                 230                 235                 240
Val Ser Pro Arg Asp Arg Pro Ser Ile Asn Ser Ile Leu Lys Arg Pro
                245                 250                 255
Phe Leu Glu Asn Leu Ile Pro Lys Tyr Leu Thr Pro Glu Val Ser Phe
            260                 265                 270
Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln Tyr Lys Leu Lys Val
        275                 280                 285
Glu Lys Gln Leu Val Ser Ser Lys Gly Tyr Leu Arg Gln Asn Leu Ser
    290                 295                 300
Ala Val Glu Leu Ile Leu Lys Asn Leu Leu Lys Ala Pro His Trp Lys
305                 310                 315                 320
Phe Ile Leu Pro Ser Pro Lys Lys Val Ser Arg Val Gly Thr Asp His
                325                 330                 335
Cys Phe Phe Arg Arg Ala Ser His Glu Ile Ala Ser Leu Tyr Ala Gln
            340                 345                 350
Phe His Met Ala Gly Glu Ala Ser Gln Ser Trp Gln Lys Ala Lys Glu
        355                 360                 365
Glu Gln Ser His Ala Leu His Glu Gly Arg Gln Glu Ser Leu Trp Glu
    370                 375                 380
Leu Leu Phe Thr Lys Pro Ser Asp Leu Leu Lys Ala Ala Val Ser His
385                 390                 395                 400
Asp Cys Ala Thr Val Pro Gln Pro Gly Ile Gln Ser Lys Thr Arg Ser
                405                 410                 415
Gln Lys Asn Lys Ala Leu Leu Thr Ser Gln Thr Gly Arg Arg Gly Lys
            420                 425                 430
Gly Ala Pro His Ile Ser Asp Asp Gly Arg Pro Gly Arg Asp Ala Pro
        435                 440                 445
His Phe Leu Asp Gly Met Ala Ala Gly Gln Arg Arg Ser Ser Leu Ser
    450                 455                 460
Arg Leu Gly Ser Gln Ala Glu Gly Leu Leu Thr Ser Gln Thr Met Gly
465                 470                 475                 480
Gly Arg Ala Glu Thr Leu Leu Thr Ser Gln Thr Gly Leu Arg Gln Glu
                485                 490                 495
Asn Cys Leu Asn Leu Gly Gly Gly Gly Cys Ser Glu Pro Arg Ser Ser
            500                 505                 510
Gly Glu Arg Gly His Pro Cys Leu Val Pro Val Phe Lys Gly Asn Ala
        515                 520                 525
Ser Ser Phe Cys Pro Phe Lys Asn Lys Asp Glu Val Arg Trp Val Arg
    530                 535                 540
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<210> 53
<211> 2559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2559)
<223> MOOSE03475

<400> 53

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gcc aaa atg aaa gtg tgg gct tta ctc cct agg ctg gat agt gag tgg   48
Ala Lys Met Lys Val Trp Ala Leu Leu Pro Arg Leu Asp Ser Glu Trp
 1               5                  10                  15

ggt atg tgt ccg ggg tgg gag tca ggg gaa ggg gga ggc aga tgg aga   96
Gly Met Cys Pro Gly Trp Glu Ser Gly Glu Gly Gly Gly Arg Trp Arg
            20                  25                  30

ggg tgg cag cct cca gct gca tta gag cct cgt gga caa cct agg gaa   144
Gly Trp Gln Pro Pro Ala Ala Leu Glu Pro Arg Gly Gln Pro Arg Glu
        35                  40                  45

cat ttc tgc atg gtt cta ggc aga ggc aga tca gcc aaa ggg aga gga   192
His Phe Cys Met Val Leu Gly Arg Gly Arg Ser Ala Lys Gly Arg Gly
    50                  55                  60

gct gaa ggt gct tgg aag ggc cag gta gga ggg tgc aga gaa tgt gga   240
Ala Glu Gly Ala Trp Lys Gly Gln Val Gly Gly Cys Arg Glu Cys Gly
65                  70                  75                  80

gaa ata gta acg gtt tta cac tgt tgg tgg gag tgt aaa ctg gtt caa   288
Glu Ile Val Thr Val Leu His Cys Trp Trp Glu Cys Lys Leu Val Gln
                85                  90                  95

cca ttg tgg aag aca gtg tgg cga ttc ctc aag gat cta gaa cta gaa   336
Pro Leu Trp Lys Thr Val Trp Arg Phe Leu Lys Asp Leu Glu Leu Glu
            100                 105                 110

ata cca ttt gac cca gca atc cca ttt ctg ggt ata tac cca aag gat   384
Ile Pro Phe Asp Pro Ala Ile Pro Phe Leu Gly Ile Tyr Pro Lys Asp
        115                 120                 125

tat aaa tca tgc tac tat aaa gac aaa tgc aca ctt cat gtc ctt tgc   432
Tyr Lys Ser Cys Tyr Tyr Lys Asp Lys Cys Thr Leu His Val Leu Cys
    130                 135                 140

agg gac atg gat gaa gat gga tac cat cat tct gag caa act gtc aca   480
Arg Asp Met Asp Glu Asp Gly Tyr His His Ser Glu Gln Thr Val Thr
145                 150                 155                 160

agg aca gaa aac caa aca ctg cat att ctc act cat agg tgg gaa ttg   528
Arg Thr Glu Asn Gln Thr Leu His Ile Leu Thr His Arg Trp Glu Leu
                165                 170                 175

aac aat gag aac att tgg aca cag ggt ggg gaa cat cac aaa cgg ggg   576
Asn Asn Glu Asn Ile Trp Thr Gln Gly Gly Glu His His Lys Arg Gly
            180                 185                 190
```

```
cct gtc atg gga tgg ggg gca ggg gga ggg ata gca tta gga gaa ata   624
Pro Val Met Gly Trp Gly Ala Gly Gly Gly Ile Ala Leu Gly Glu Ile
        195                 200                 205

cct aat gta aat gac gag tta atg ggt gca gca aac caa cat ggc aca   672
Pro Asn Val Asn Asp Glu Leu Met Gly Ala Ala Asn Gln His Gly Thr
    210                 215                 220

tgt ata cct atg tat caa acc tgc acc tta ata tgc aaa tgt ctc act   720
Cys Ile Pro Met Tyr Gln Thr Cys Thr Leu Ile Cys Lys Cys Leu Thr
225                 230                 235                 240

ttt gat ttt tct tta gtt ttg cta ctt gag aag ata gaa cat gat gac   768
Phe Asp Phe Ser Leu Val Leu Leu Leu Glu Lys Ile Glu His Asp Asp
                245                 250                 255

atc tgc aat aaa act ttg aag att aca gat ttt ggg ttg gcg agg gaa   816
Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu Ala Arg Glu
            260                 265                 270

tgg cac agg acc acc aaa atg agc aca gca ggc acc tat gcc tgg atg   864
Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr Ala Trp Met
        275                 280                 285

gcc ccc gaa gtg atc aag tct tcc ttg ttt tct aag gga agc gac atc   912
Ala Pro Glu Val Ile Lys Ser Ser Leu Phe Ser Lys Gly Ser Asp Ile
    290                 295                 300

tgg agc tat gga gtg ctg ctg tgg gaa ctg ctc acc gga gaa gtc ccc   960
Trp Ser Tyr Gly Val Leu Leu Trp Glu Leu Leu Thr Gly Glu Val Pro
305                 310                 315                 320

tat cgg ggc att gat ggc ctc gcc gtg gct tat ggg gta gca gtc aat   1008
Tyr Arg Gly Ile Asp Gly Leu Ala Val Ala Tyr Gly Val Ala Val Asn
                325                 330                 335

aaa ctc act ttg ccc att cca tcc acc tgc cct gag ccg ttt gcc aag   1056
Lys Leu Thr Leu Pro Ile Pro Ser Thr Cys Pro Glu Pro Phe Ala Lys
            340                 345                 350

ctc atg aaa gaa tgc tgg caa caa gac cct cat att cgt cca tcg ttt   1104
Leu Met Lys Glu Cys Trp Gln Gln Asp Pro His Ile Arg Pro Ser Phe
        355                 360                 365

gcc tta att ctc gaa cag ttg act gct att gaa ggg gca gtg atg act   1152
Ala Leu Ile Leu Glu Gln Leu Thr Ala Ile Glu Gly Ala Val Met Thr
    370                 375                 380

gag atg cct caa gaa tct ttt cat tcc atg caa gat gac tgg aaa cta   1200
Glu Met Pro Gln Glu Ser Phe His Ser Met Gln Asp Asp Trp Lys Leu
385                 390                 395                 400

gaa att caa caa atg ttt gat gag ttg aga aca aag gaa aag gag ctg   1248
Glu Ile Gln Gln Met Phe Asp Glu Leu Arg Thr Lys Glu Lys Glu Leu
                405                 410                 415

cga tcc cgg gaa gag gag ctg act cgg gcg gct ctg cag cag aag tct   1296
Arg Ser Arg Glu Glu Glu Leu Thr Arg Ala Ala Leu Gln Gln Lys Ser
            420                 425                 430
```

```
cag gag gag ctg cta aag cgg cgt gag cag cag ctg gca gag cgc gag   1344
Gln Glu Glu Leu Leu Lys Arg Arg Glu Gln Gln Leu Ala Glu Arg Glu
        435                 440                 445

atc gac gtg ctg gag cgg gaa ctt aac att ctg ata ttc cag cta aac   1392
Ile Asp Val Leu Glu Arg Glu Leu Asn Ile Leu Ile Phe Gln Leu Asn
    450                 455                 460

cag gag aag ccc aag gta aag aag agg aag ggc aag ttt aag aga agt   1440
Gln Glu Lys Pro Lys Val Lys Lys Arg Lys Gly Lys Phe Lys Arg Ser
465                 470                 475                 480

cgt tta aag ctc aaa gat gga cat cga atc agt tta cct tca gat ttc   1488
Arg Leu Lys Leu Lys Asp Gly His Arg Ile Ser Leu Pro Ser Asp Phe
                485                 490                 495

cag cac aag ata acc gtg cag gcc tct ccc aac ttg gac aaa cgg cgg   1536
Gln His Lys Ile Thr Val Gln Ala Ser Pro Asn Leu Asp Lys Arg Arg
            500                 505                 510

agc ctg aac agc agc agt tcc agt ccc ccg agc agc ccc aca atg atg   1584
Ser Leu Asn Ser Ser Ser Ser Ser Pro Pro Ser Ser Pro Thr Met Met
        515                 520                 525

ccc cga ctc cga gcc ata cag ttg act tca gat gaa agc aat aaa act   1632
Pro Arg Leu Arg Ala Ile Gln Leu Thr Ser Asp Glu Ser Asn Lys Thr
    530                 535                 540

tgg gga agg aac aca gtc ttt cga caa gaa gaa ttt gag gat gta aaa   1680
Trp Gly Arg Asn Thr Val Phe Arg Gln Glu Glu Phe Glu Asp Val Lys
545                 550                 555                 560

agg aat ttt aag aaa aaa ggt tgt acc tgg gga cca aat tcc att caa   1728
Arg Asn Phe Lys Lys Lys Gly Cys Thr Trp Gly Pro Asn Ser Ile Gln
                565                 570                 575

atg aaa gat aga aca gat tgc aaa gaa agg tac gcc tac att gat cta   1776
Met Lys Asp Arg Thr Asp Cys Lys Glu Arg Tyr Ala Tyr Ile Asp Leu
            580                 585                 590

cct ctt ggg aaa gat gct cag aga gag aat cct gca gaa gct gaa agc   1824
Pro Leu Gly Lys Asp Ala Gln Arg Glu Asn Pro Ala Glu Ala Glu Ser
        595                 600                 605

tgg gag gag gca gcc tct gcg aat gct gcc aca gtc tcc att gag atg   1872
Trp Glu Glu Ala Ala Ser Ala Asn Ala Ala Thr Val Ser Ile Glu Met
    610                 615                 620

act cct acg aat agt ctg agt aga tcc ccc cag aga aag aaa acg gag   1920
Thr Pro Thr Asn Ser Leu Ser Arg Ser Pro Gln Arg Lys Lys Thr Glu
625                 630                 635                 640

tca gct ctg tat ggg tgc acc gtc ctt ctg gca tcg gtg gct ctg gga   1968
Ser Ala Leu Tyr Gly Cys Thr Val Leu Leu Ala Ser Val Ala Leu Gly
                645                 650                 655

ctg gac ctc aga gag ctt cat aaa gca cag gct gct gaa gaa ccg ttg   2016
Leu Asp Leu Arg Glu Leu His Lys Ala Gln Ala Ala Glu Glu Pro Leu
            660                 665                 670
```

```
ccc aag gaa gag aag aag aaa cga gag gga atc ttc cag cgg gct tcc   2064
Pro Lys Glu Glu Lys Lys Lys Arg Glu Gly Ile Phe Gln Arg Ala Ser
        675                 680                 685

aag tcc cgc aga agc gcc agt cct ccc aca agc ctg cca tcc acc tgt   2112
Lys Ser Arg Arg Ser Ala Ser Pro Pro Thr Ser Leu Pro Ser Thr Cys
    690                 695                 700

ggg gag gcc agc agc cca ccc tcc ctg cca ctg tca agt gcc ctg ggc   2160
Gly Glu Ala Ser Ser Pro Pro Ser Leu Pro Leu Ser Ser Ala Leu Gly
705                 710                 715                 720

atc ctc tcc aca cct tct ttc tcc aca aag tgc ctg ctg cag atg gac   2208
Ile Leu Ser Thr Pro Ser Phe Ser Thr Lys Cys Leu Leu Gln Met Asp
                725                 730                 735

agt gaa gat cca ctg gtg gac agt gca cct gtc act tgt gac tct gag   2256
Ser Glu Asp Pro Leu Val Asp Ser Ala Pro Val Thr Cys Asp Ser Glu
            740                 745                 750

atg ctc act ccg gat ttt tgt ccc act gcc cca gga agt ggt cgt gag   2304
Met Leu Thr Pro Asp Phe Cys Pro Thr Ala Pro Gly Ser Gly Arg Glu
        755                 760                 765

cca gcc ctc atg cca aga ctt gac act gat tgt agt gta tca aga aac   2352
Pro Ala Leu Met Pro Arg Leu Asp Thr Asp Cys Ser Val Ser Arg Asn
    770                 775                 780

ttg ccg tct tcc ttc cta cag cag aca tgt ggg aat gta cct tac tgt   2400
Leu Pro Ser Ser Phe Leu Gln Gln Thr Cys Gly Asn Val Pro Tyr Cys
785                 790                 795                 800

gct tct tca aaa cat aga ccg tca cat cac aga cgg acc atg tct gat   2448
Ala Ser Ser Lys His Arg Pro Ser His His Arg Arg Thr Met Ser Asp
                805                 810                 815

gga aat ccg acc cca agt gat cag cct gct agg gct gcc ata aca gag   2496
Gly Asn Pro Thr Pro Ser Asp Gln Pro Ala Arg Ala Ala Ile Thr Glu
            820                 825                 830

tgc cac agc atg gag aga tgt tca gca caa act cat tgt cca gca gtt   2544
Cys His Ser Met Glu Arg Cys Ser Ala Gln Thr His Cys Pro Ala Val
        835                 840                 845

cca gag gct gga agt                                              2559
Pro Glu Ala Gly Ser
    850
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<210> 54
<211> 853
<212> PRT
<213> Homo sapiens

<400> 54

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Ala Lys Met Lys Val Trp Ala Leu Leu Pro Arg Leu Asp Ser Glu Trp
 1               5                  10                  15
Gly Met Cys Pro Gly Trp Glu Ser Gly Glu Gly Gly Gly Arg Trp Arg
            20                  25                  30
Gly Trp Gln Pro Pro Ala Ala Leu Glu Pro Arg Gly Gln Pro Arg Glu
        35                  40                  45
```

```
His Phe Cys Met Val Leu Gly Arg Gly Arg Ser Ala Lys Gly Arg Gly
    50                  55                  60
Ala Glu Gly Ala Trp Lys Gly Gln Val Gly Gly Cys Arg Glu Cys Gly
65                  70                  75                  80
Glu Ile Val Thr Val Leu His Cys Trp Trp Glu Cys Lys Leu Val Gln
                85                  90                  95
Pro Leu Trp Lys Thr Val Trp Arg Phe Leu Lys Asp Leu Glu Leu Glu
            100                 105                 110
Ile Pro Phe Asp Pro Ala Ile Pro Phe Leu Gly Ile Tyr Pro Lys Asp
        115                 120                 125
Tyr Lys Ser Cys Tyr Tyr Lys Asp Lys Cys Thr Leu His Val Leu Cys
    130                 135                 140
Arg Asp Met Asp Glu Asp Gly Tyr His His Ser Glu Gln Thr Val Thr
145                 150                 155                 160
Arg Thr Glu Asn Gln Thr Leu His Ile Leu Thr His Arg Trp Glu Leu
                165                 170                 175
Asn Asn Glu Asn Ile Trp Thr Gln Gly Gly Glu His His Lys Arg Gly
            180                 185                 190
Pro Val Met Gly Trp Gly Ala Gly Gly Gly Ile Ala Leu Gly Glu Ile
        195                 200                 205
Pro Asn Val Asn Asp Glu Leu Met Gly Ala Ala Asn Gln His Gly Thr
    210                 215                 220
Cys Ile Pro Met Tyr Gln Thr Cys Thr Leu Ile Cys Lys Cys Leu Thr
225                 230                 235                 240
Phe Asp Phe Ser Leu Val Leu Leu Leu Glu Lys Ile Glu His Asp Asp
                245                 250                 255
Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu Ala Arg Glu
            260                 265                 270
Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr Ala Trp Met
        275                 280                 285
Ala Pro Glu Val Ile Lys Ser Ser Leu Phe Ser Lys Gly Ser Asp Ile
    290                 295                 300
Trp Ser Tyr Gly Val Leu Leu Trp Glu Leu Leu Thr Gly Glu Val Pro
305                 310                 315                 320
Tyr Arg Gly Ile Asp Gly Leu Ala Val Ala Tyr Gly Val Ala Val Asn
                325                 330                 335
Lys Leu Thr Leu Pro Ile Pro Ser Thr Cys Pro Glu Pro Phe Ala Lys
            340                 345                 350
Leu Met Lys Glu Cys Trp Gln Gln Asp Pro His Ile Arg Pro Ser Phe
        355                 360                 365
Ala Leu Ile Leu Glu Gln Leu Thr Ala Ile Glu Gly Ala Val Met Thr
    370                 375                 380
Glu Met Pro Gln Glu Ser Phe His Ser Met Gln Asp Asp Trp Lys Leu
385                 390                 395                 400
Glu Ile Gln Gln Met Phe Asp Glu Leu Arg Thr Lys Glu Lys Glu Leu
                405                 410                 415
Arg Ser Arg Glu Glu Glu Leu Thr Arg Ala Ala Leu Gln Gln Lys Ser
            420                 425                 430
Gln Glu Glu Leu Leu Lys Arg Arg Glu Gln Gln Leu Ala Glu Arg Glu
        435                 440                 445
Ile Asp Val Leu Glu Arg Glu Leu Asn Ile Leu Ile Phe Gln Leu Asn
    450                 455                 460
Gln Glu Lys Pro Lys Val Lys Lys Arg Lys Gly Lys Phe Lys Arg Ser
465                 470                 475                 480
Arg Leu Lys Leu Lys Asp Gly His Arg Ile Ser Leu Pro Ser Asp Phe
                485                 490                 495
Gln His Lys Ile Thr Val Gln Ala Ser Pro Asn Leu Asp Lys Arg Arg
            500                 505                 510
Ser Leu Asn Ser Ser Ser Ser Ser Pro Pro Ser Ser Pro Thr Met Met
        515                 520                 525
Pro Arg Leu Arg Ala Ile Gln Leu Thr Ser Asp Glu Ser Asn Lys Thr
    530                 535                 540
```

```
Trp Gly Arg Asn Thr Val Phe Arg Gln Glu Glu Phe Glu Asp Val Lys
545                 550                 555                 560
Arg Asn Phe Lys Lys Lys Gly Cys Thr Trp Gly Pro Asn Ser Ile Gln
                565                 570                 575
Met Lys Asp Arg Thr Asp Cys Lys Glu Arg Tyr Ala Tyr Ile Asp Leu
            580                 585                 590
Pro Leu Gly Lys Asp Ala Gln Arg Glu Asn Pro Ala Glu Ala Glu Ser
        595                 600                 605
Trp Glu Glu Ala Ala Ser Ala Asn Ala Ala Thr Val Ser Ile Glu Met
    610                 615                 620
Thr Pro Thr Asn Ser Leu Ser Arg Ser Pro Gln Arg Lys Lys Thr Glu
625                 630                 635                 640
Ser Ala Leu Tyr Gly Cys Thr Val Leu Leu Ala Ser Val Ala Leu Gly
                645                 650                 655
Leu Asp Leu Arg Glu Leu His Lys Ala Gln Ala Ala Glu Glu Pro Leu
            660                 665                 670
Pro Lys Glu Glu Lys Lys Lys Arg Glu Gly Ile Phe Gln Arg Ala Ser
        675                 680                 685
Lys Ser Arg Arg Ser Ala Ser Pro Pro Thr Ser Leu Pro Ser Thr Cys
    690                 695                 700
Gly Glu Ala Ser Ser Pro Pro Ser Leu Pro Leu Ser Ser Ala Leu Gly
705                 710                 715                 720
Ile Leu Ser Thr Pro Ser Phe Ser Thr Lys Cys Leu Leu Gln Met Asp
                725                 730                 735
Ser Glu Asp Pro Leu Val Asp Ser Ala Pro Val Thr Cys Asp Ser Glu
            740                 745                 750
Met Leu Thr Pro Asp Phe Cys Pro Thr Ala Pro Gly Ser Gly Arg Glu
        755                 760                 765
Pro Ala Leu Met Pro Arg Leu Asp Thr Asp Cys Ser Val Ser Arg Asn
    770                 775                 780
Leu Pro Ser Ser Phe Leu Gln Gln Thr Cys Gly Asn Val Pro Tyr Cys
785                 790                 795                 800
Ala Ser Ser Lys His Arg Pro Ser His His Arg Arg Thr Met Ser Asp
                805                 810                 815
Gly Asn Pro Thr Pro Ser Asp Gln Pro Ala Arg Ala Ala Ile Thr Glu
            820                 825                 830
Cys His Ser Met Glu Arg Cys Ser Ala Gln Thr His Cys Pro Ala Val
        835                 840                 845
Pro Glu Ala Gly Ser
    850
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<210> 55
<211> 2625
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2625)
<223> MOOSE03605

<400> 55

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gtc tca ctc cag ccc agg ctg gag tgc agt ggt gca atc tca gct cat   48
Val Ser Leu Gln Pro Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala His
 1               5                  10                  15

tgc aac ctc tgc ctc tct tgc tca ggt gat ctt ccc acc tca gtc gcc   96
Cys Asn Leu Cys Leu Ser Cys Ser Gly Asp Leu Pro Thr Ser Val Ala
            20                  25                  30
```

```
caa agg gaa tgc cag gct ggg gaa gtt tta caa tgt tta ata ggt tgg   144
Gln Arg Glu Cys Gln Ala Gly Glu Val Leu Gln Cys Leu Ile Gly Trp
         35                  40                  45

gca ggg aag acc tcc ctg aga ggg tgg cct gag gga gag agg aag aaa   192
Ala Gly Lys Thr Ser Leu Arg Gly Trp Pro Glu Gly Glu Arg Lys Lys
     50                  55                  60

act gtg cag acg ttt gga aga agt gag ttc cag gaa gaa gaa aca gca   240
Thr Val Gln Thr Phe Gly Arg Ser Glu Phe Gln Glu Glu Glu Thr Ala
 65                  70                  75                  80

agt tca ttt tcc tgg aga cgg gag cat gcc tca tgt gtt ctt cat gca   288
Ser Ser Phe Ser Trp Arg Arg Glu His Ala Ser Cys Val Leu His Ala
                 85                  90                  95

tct gct aga att ttt act tgc atg ttt tac tct gga gtg gag tgg cgc   336
Ser Ala Arg Ile Phe Thr Cys Met Phe Tyr Ser Gly Val Glu Trp Arg
            100                 105                 110

gat ctc ggt tca ctg caa cct cca cct ccc ggg ttc aag cga ttc tcc   384
Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser
        115                 120                 125

tgc ctc agc ctc cca agt agc tgg gac tac agg tcc ctg cca cca tgc   432
Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ser Leu Pro Pro Cys
    130                 135                 140

ctg gct aat ttt tgt att ttt aga gat aaa acc aaa ggt gca aaa gtg   480
Leu Ala Asn Phe Cys Ile Phe Arg Asp Lys Thr Lys Gly Ala Lys Val
145                 150                 155                 160

gtt gaa act cag gga tgg gag gag gaa gca gag gat ttc tat ttc aat   528
Val Glu Thr Gln Gly Trp Glu Glu Glu Ala Glu Asp Phe Tyr Phe Asn
                165                 170                 175

tat aag cct tgt agt act tgg cct cca gct gct tct tca ttt tct cca   576
Tyr Lys Pro Cys Ser Thr Trp Pro Pro Ala Ala Ser Ser Phe Ser Pro
            180                 185                 190

ggg ctt ccc tgt gac tgt gga tca ggc cat tgc act cca gtc tgc act   624
Gly Leu Pro Cys Asp Cys Gly Ser Gly His Cys Thr Pro Val Cys Thr
        195                 200                 205

gca cct ggt ggt ttg ata ttt tta atc ttt act gat ttt ttt gag tta   672
Ala Pro Gly Gly Leu Ile Phe Leu Ile Phe Thr Asp Phe Phe Glu Leu
    210                 215                 220

ttt tta gaa tgg gag gca atg cca ctc tgt ggg cag tgt agc cta ggg   720
Phe Leu Glu Trp Glu Ala Met Pro Leu Cys Gly Gln Cys Ser Leu Gly
225                 230                 235                 240

cct agg agg tgt cat cat tgt tct cat ttt aca cac ggg gaa act gag   768
Pro Arg Arg Cys His His Cys Ser His Phe Thr His Gly Glu Thr Glu
                245                 250                 255

gct cag gga gta aga tca ctt gct tct ggg att aca gat gca tgc cac   816
Ala Gln Gly Val Arg Ser Leu Ala Ser Gly Ile Thr Asp Ala Cys His
            260                 265                 270
```

```
cac gcc cag cta act ttt gta ttt tta gta cag acg ggg ctt cac cat   864
His Ala Gln Leu Thr Phe Val Phe Leu Val Gln Thr Gly Leu His His
        275                 280                 285

gtt ggc cag gct ggt ctc aat ctc ttg act tca ggt gat ctg ccc cct   912
Val Gly Gln Ala Gly Leu Asn Leu Leu Thr Ser Gly Asp Leu Pro Pro
    290                 295                 300

cgg cct ctc caa atc cgc agg gac cga gtg gaa ccc cag agc gtg tcc   960
Arg Pro Leu Gln Ile Arg Arg Asp Arg Val Glu Pro Gln Ser Val Ser
305                 310                 315                 320

ctg tcg tgg cgg gag ccc atc cct gcc gga gcc cct ggg gcc aat gac   1008
Leu Ser Trp Arg Glu Pro Ile Pro Ala Gly Ala Pro Gly Ala Asn Asp
                325                 330                 335

acg gag tac gag atc cga tac tac gag aag ggt cag agt gag cag act   1056
Thr Glu Tyr Glu Ile Arg Tyr Tyr Glu Lys Gly Gln Ser Glu Gln Thr
            340                 345                 350

tac tcc atg gtg aag aca ggg gcg ccc aca gtc acc gtc acc aac ctg   1104
Tyr Ser Met Val Lys Thr Gly Ala Pro Thr Val Thr Val Thr Asn Leu
        355                 360                 365

aag ccg gct acc cgc tac gtc ttt cag atc cgg gcc gct tcc ccg ggg   1152
Lys Pro Ala Thr Arg Tyr Val Phe Gln Ile Arg Ala Ala Ser Pro Gly
    370                 375                 380

cca tcc tgg gag gcc cag agt ttt aac ccc agc att gaa gta cag acc   1200
Pro Ser Trp Glu Ala Gln Ser Phe Asn Pro Ser Ile Glu Val Gln Thr
385                 390                 395                 400

ctg ggg gag ggt aag gac cag agc ccc gcc att gtc gtc acc gta gtg   1248
Leu Gly Glu Gly Lys Asp Gln Ser Pro Ala Ile Val Val Thr Val Val
                405                 410                 415

acc atc tcg gcc ctc ctc gtc ctg ggc tcc gtg atg agt gct ctg aga   1296
Thr Ile Ser Ala Leu Leu Val Leu Gly Ser Val Met Ser Ala Leu Arg
            420                 425                 430

ggc aga agg agg aaa ggg aga caa gca agc caa gag ccc ctc ttc cgg   1344
Gly Arg Arg Arg Lys Gly Arg Gln Ala Ser Gln Glu Pro Leu Phe Arg
        435                 440                 445

gca gag gct ctg cag gac agg agc gcc cca ggg aca gtc cca aca cgt   1392
Ala Glu Ala Leu Gln Asp Arg Ser Ala Pro Gly Thr Val Pro Thr Arg
    450                 455                 460

cgc aca ttc ctg gac ccc cag agc tgt ggg gac ctg ctg cag gct gtg   1440
Arg Thr Phe Leu Asp Pro Gln Ser Cys Gly Asp Leu Leu Gln Ala Val
465                 470                 475                 480

cat ctg ttc gcc aag gaa ctg gat gcg aaa agc gtc acg ctg gag agg   1488
His Leu Phe Ala Lys Glu Leu Asp Ala Lys Ser Val Thr Leu Glu Arg
                485                 490                 495

agc ctt gga gga ggc aag ctg ggc gcc cag gaa gcc ttg tgc tgt ttc   1536
Ser Leu Gly Gly Gly Lys Leu Gly Ala Gln Glu Ala Leu Cys Cys Phe
            500                 505                 510
```

```
ccc aca ggg cgg ttt ggg gag ctg tgc tgt ggc tgc ttg cag ctc ccc   1584
Pro Thr Gly Arg Phe Gly Glu Leu Cys Cys Gly Cys Leu Gln Leu Pro
        515                 520                 525

ggt cgc cag gag ctg ctc gta gcc gtg cat atg ctg agg gac agc gcc   1632
Gly Arg Gln Glu Leu Leu Val Ala Val His Met Leu Arg Asp Ser Ala
    530                 535                 540

tcc gac tca cag agg ctc ggc ttc ctg gcc gag gcc ctc acg ctg ggc   1680
Ser Asp Ser Gln Arg Leu Gly Phe Leu Ala Glu Ala Leu Thr Leu Gly
545                 550                 555                 560

cag ttt gac cat agc cac atc gtg cgg ctg gag ggc gtt gtt acc cga   1728
Gln Phe Asp His Ser His Ile Val Arg Leu Glu Gly Val Val Thr Arg
                565                 570                 575

ggt agg gcc cgc acc ttg atg att gtc acc gag tac atg agc cat ggg   1776
Gly Arg Ala Arg Thr Leu Met Ile Val Thr Glu Tyr Met Ser His Gly
            580                 585                 590

gcc ctg gac ggc ttc ctc agg cgg cac gag ggg cag ctg gtg gct ggg   1824
Ala Leu Asp Gly Phe Leu Arg Arg His Glu Gly Gln Leu Val Ala Gly
        595                 600                 605

caa ctg atg ggg ttg ctg cct ggg ctg gca tca gcc atg aag tat ctg   1872
Gln Leu Met Gly Leu Leu Pro Gly Leu Ala Ser Ala Met Lys Tyr Leu
    610                 615                 620

tca gag atg ggc tac gtt cac cgg ggc ctg gca gct cgc cat gtg ctg   1920
Ser Glu Met Gly Tyr Val His Arg Gly Leu Ala Ala Arg His Val Leu
625                 630                 635                 640

gtc agc agc gac ctt gtc tgc aag atc tct ggc ttc ggg cgg ggc ccc   1968
Val Ser Ser Asp Leu Val Cys Lys Ile Ser Gly Phe Gly Arg Gly Pro
                645                 650                 655

cgg gac cga tca gag gct gtc tac acc act atg agt ggc cgg agc cca   2016
Arg Asp Arg Ser Glu Ala Val Tyr Thr Thr Met Ser Gly Arg Ser Pro
            660                 665                 670

gcg cta tgg gcc gct ccc gag aca ctt cag ttt ggc cac ttc agc tct   2064
Ala Leu Trp Ala Ala Pro Glu Thr Leu Gln Phe Gly His Phe Ser Ser
        675                 680                 685

gcc agt gac gtg tgg agc ttc ggc atc atc atg tgg gag gtg atg gcc   2112
Ala Ser Asp Val Trp Ser Phe Gly Ile Ile Met Trp Glu Val Met Ala
    690                 695                 700

ttt ggg gag cgg cct tac tgg gac atg tct ggc caa gac gtg atc aag   2160
Phe Gly Glu Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val Ile Lys
705                 710                 715                 720

gct gtg gag gat ggc ttc cgg ctg cca ccc ccc agg aac tgt cct aac   2208
Ala Val Glu Asp Gly Phe Arg Leu Pro Pro Pro Arg Asn Cys Pro Asn
                725                 730                 735

ctt ctg cac cga cta atg ctc gac tgc tgg cag aag gac cca ggt gag   2256
Leu Leu His Arg Leu Met Leu Asp Cys Trp Gln Lys Asp Pro Gly Glu
            740                 745                 750
```

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cgg ccc agg ttc tcc cag atc cac agc atc ctg agc aag atg gtg cag   2304
Arg Pro Arg Phe Ser Gln Ile His Ser Ile Leu Ser Lys Met Val Gln
        755                 760                 765

gac cca gag ccc ccc aag tat ccc agc tgt cgg ttg agc aca gct cct   2352
Asp Pro Glu Pro Pro Lys Tyr Pro Ser Cys Arg Leu Ser Thr Ala Pro
    770                 775                 780

ctg acc cgc agg cct ccc acc cca cta gcg gac cgt gcc ttc tcc acc   2400
Leu Thr Arg Arg Pro Pro Thr Pro Leu Ala Asp Arg Ala Phe Ser Thr
785                 790                 795                 800

ttc ccc tcc ttt ggc tct gtg ggc gcg tgg ctg gag gcc ctg gac ctg   2448
Phe Pro Ser Phe Gly Ser Val Gly Ala Trp Leu Glu Ala Leu Asp Leu
                805                 810                 815

tgc cgc tac aag gac agc ttc gcg gct gct ggc tat ggg agc ctg gag   2496
Cys Arg Tyr Lys Asp Ser Phe Ala Ala Ala Gly Tyr Gly Ser Leu Glu
            820                 825                 830

gcc gtg gcc gag atg act gcc cag gac ctg gtg agc cta ggc atc tct   2544
Ala Val Ala Glu Met Thr Ala Gln Asp Leu Val Ser Leu Gly Ile Ser
        835                 840                 845

ttg gct gaa cat cga gag gcc ctc ctc agc ggg atc agc gcc ctg cag   2592
Leu Ala Glu His Arg Glu Ala Leu Leu Ser Gly Ile Ser Ala Leu Gln
    850                 855                 860

gca cga gtg ctc cag ctg cag ggc cag ggg gtg                       2625
Ala Arg Val Leu Gln Leu Gln Gly Gln Gly Val
865                 870                 875
```

<210> 56
<211> 875
<212> PRT
<213> Homo sapiens

<400> 56

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Val Ser Leu Gln Pro Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala His
 1               5                  10                  15
Cys Asn Leu Cys Leu Ser Cys Ser Gly Asp Leu Pro Thr Ser Val Ala
            20                  25                  30
Gln Arg Glu Cys Gln Ala Gly Glu Val Leu Gln Cys Leu Ile Gly Trp
        35                  40                  45
Ala Gly Lys Thr Ser Leu Arg Gly Trp Pro Glu Gly Glu Arg Lys Lys
    50                  55                  60
Thr Val Gln Thr Phe Gly Arg Ser Glu Phe Gln Glu Glu Glu Thr Ala
65                  70                  75                  80
Ser Ser Phe Ser Trp Arg Arg Glu His Ala Ser Cys Val Leu His Ala
                85                  90                  95
Ser Ala Arg Ile Phe Thr Cys Met Phe Tyr Ser Gly Val Glu Trp Arg
            100                 105                 110
Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser
        115                 120                 125
Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ser Leu Pro Pro Cys
    130                 135                 140
Leu Ala Asn Phe Cys Ile Phe Arg Asp Lys Thr Lys Gly Ala Lys Val
145                 150                 155                 160
Val Glu Thr Gln Gly Trp Glu Glu Glu Ala Glu Asp Phe Tyr Phe Asn
                165                 170                 175
```

```
Tyr Lys Pro Cys Ser Thr Trp Pro Pro Ala Ala Ser Ser Phe Ser Pro
            180                 185                 190
Gly Leu Pro Cys Asp Cys Gly Ser Gly His Cys Thr Pro Val Cys Thr
        195                 200                 205
Ala Pro Gly Gly Leu Ile Phe Leu Ile Phe Thr Asp Phe Phe Glu Leu
    210                 215                 220
Phe Leu Glu Trp Glu Ala Met Pro Leu Cys Gly Gln Cys Ser Leu Gly
225                 230                 235                 240
Pro Arg Arg Cys His His Cys Ser His Phe Thr His Gly Glu Thr Glu
                245                 250                 255
Ala Gln Gly Val Arg Ser Leu Ala Ser Gly Ile Thr Asp Ala Cys His
            260                 265                 270
His Ala Gln Leu Thr Phe Val Phe Leu Val Gln Thr Gly Leu His His
        275                 280                 285
Val Gly Gln Ala Gly Leu Asn Leu Leu Thr Ser Gly Asp Leu Pro Pro
    290                 295                 300
Arg Pro Leu Gln Ile Arg Arg Asp Arg Val Glu Pro Gln Ser Val Ser
305                 310                 315                 320
Leu Ser Trp Arg Glu Pro Ile Pro Ala Gly Ala Pro Gly Ala Asn Asp
                325                 330                 335
Thr Glu Tyr Glu Ile Arg Tyr Tyr Glu Lys Gly Gln Ser Glu Gln Thr
            340                 345                 350
Tyr Ser Met Val Lys Thr Gly Ala Pro Thr Val Thr Val Thr Asn Leu
        355                 360                 365
Lys Pro Ala Thr Arg Tyr Val Phe Gln Ile Arg Ala Ala Ser Pro Gly
    370                 375                 380
Pro Ser Trp Glu Ala Gln Ser Phe Asn Pro Ser Ile Glu Val Gln Thr
385                 390                 395                 400
Leu Gly Glu Gly Lys Asp Gln Ser Pro Ala Ile Val Val Thr Val Val
                405                 410                 415
Thr Ile Ser Ala Leu Leu Val Leu Gly Ser Val Met Ser Ala Leu Arg
            420                 425                 430
Gly Arg Arg Arg Lys Gly Arg Gln Ala Ser Gln Glu Pro Leu Phe Arg
        435                 440                 445
Ala Glu Ala Leu Gln Asp Arg Ser Ala Pro Gly Thr Val Pro Thr Arg
    450                 455                 460
Arg Thr Phe Leu Asp Pro Gln Ser Cys Gly Asp Leu Leu Gln Ala Val
465                 470                 475                 480
His Leu Phe Ala Lys Glu Leu Asp Ala Lys Ser Val Thr Leu Glu Arg
                485                 490                 495
Ser Leu Gly Gly Gly Lys Leu Gly Ala Gln Glu Ala Leu Cys Cys Phe
            500                 505                 510
Pro Thr Gly Arg Phe Gly Glu Leu Cys Cys Gly Cys Leu Gln Leu Pro
        515                 520                 525
Gly Arg Gln Glu Leu Leu Val Ala Val His Met Leu Arg Asp Ser Ala
    530                 535                 540
Ser Asp Ser Gln Arg Leu Gly Phe Leu Ala Glu Ala Leu Thr Leu Gly
545                 550                 555                 560
Gln Phe Asp His Ser His Ile Val Arg Leu Glu Gly Val Val Thr Arg
                565                 570                 575
Gly Arg Ala Arg Thr Leu Met Ile Val Thr Glu Tyr Met Ser His Gly
            580                 585                 590
Ala Leu Asp Gly Phe Leu Arg Arg His Glu Gly Gln Leu Val Ala Gly
        595                 600                 605
Gln Leu Met Gly Leu Leu Pro Gly Leu Ala Ser Ala Met Lys Tyr Leu
    610                 615                 620
Ser Glu Met Gly Tyr Val His Arg Gly Leu Ala Ala Arg His Val Leu
625                 630                 635                 640
Val Ser Ser Asp Leu Val Cys Lys Ile Ser Gly Phe Gly Arg Gly Pro
                645                 650                 655
Arg Asp Arg Ser Glu Ala Val Tyr Thr Thr Met Ser Gly Arg Ser Pro
            660                 665                 670
```

```
Ala Leu Trp Ala Ala Pro Glu Thr Leu Gln Phe Gly His Phe Ser Ser
        675                 680                 685
Ala Ser Asp Val Trp Ser Phe Gly Ile Ile Met Trp Glu Val Met Ala
    690                 695                 700
Phe Gly Glu Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val Ile Lys
705                 710                 715                 720
Ala Val Glu Asp Gly Phe Arg Leu Pro Pro Pro Arg Asn Cys Pro Asn
                725                 730                 735
Leu Leu His Arg Leu Met Leu Asp Cys Trp Gln Lys Asp Pro Gly Glu
            740                 745                 750
Arg Pro Arg Phe Ser Gln Ile His Ser Ile Leu Ser Lys Met Val Gln
        755                 760                 765
Asp Pro Glu Pro Pro Lys Tyr Pro Ser Cys Arg Leu Ser Thr Ala Pro
    770                 775                 780
Leu Thr Arg Arg Pro Pro Thr Pro Leu Ala Asp Arg Ala Phe Ser Thr
785                 790                 795                 800
Phe Pro Ser Phe Gly Ser Val Gly Ala Trp Leu Glu Ala Leu Asp Leu
                805                 810                 815
Cys Arg Tyr Lys Asp Ser Phe Ala Ala Ala Gly Tyr Gly Ser Leu Glu
            820                 825                 830
Ala Val Ala Glu Met Thr Ala Gln Asp Leu Val Ser Leu Gly Ile Ser
        835                 840                 845
Leu Ala Glu His Arg Glu Ala Leu Leu Ser Gly Ile Ser Ala Leu Gln
    850                 855                 860
Ala Arg Val Leu Gln Leu Gln Gly Gln Gly Val
865                 870                 875


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<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2631)
<223> MOOSE03608

<400> 57
gtt gca agt cgg tgg aga cgt acc ctt ggt gct caa ccc ctg tcc gtt   48
Val Ala Ser Arg Trp Arg Arg Thr Leu Gly Ala Gln Pro Leu Ser Val
 1               5                  10                  15

tgt ttg ttt gtt tgt ttt gtt ttg ttt tgt ctt ctt aga cat agt ctt   96
Cys Leu Phe Val Cys Phe Val Leu Phe Cys Leu Leu Arg His Ser Leu
            20                  25                  30

gct ctg tcg ccc agg ctg gcg tgc aat gaa acg cta atg gac tcc act   144
Ala Leu Ser Pro Arg Leu Ala Cys Asn Glu Thr Leu Met Asp Ser Thr
        35                  40                  45

aca gcg act gct gag ctg ggc tgg atg gtg cat cct cca tca ggg tgg   192
Thr Ala Thr Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp
    50                  55                  60

gaa gag gtg agt ggc tac gat gag aac atg aac acg atc cgc acg tac   240
Glu Glu Val Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr
65                  70                  75                  80

cag gtg tgc aac gtg ttt gag tca agc cag aac aac tgg cta cgg acc   288
Gln Val Cys Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr
                85                  90                  95
```

```
aag ttt atc cgg cgc cgt ggc gcc cac cgc atc cac gtg gag atg aag   336
Lys Phe Ile Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys
            100                 105                 110

ttt tcg gtg cgt gac tgc agc agc atc ccc agc gtg cct ggc tcc tgc   384
Phe Ser Val Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys
        115                 120                 125

aag gag acc ttc aac ctc tat tac tat gag gct gac ttt gac tcg gcc   432
Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala
    130                 135                 140

acc aag acc ttc ccc aac tgg atg gag aat cca tgg gtg aag gtg gat   480
Thr Lys Thr Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp
145                 150                 155                 160

acc att gca gcc gac gag agc ttc tcc cag gtg gac ctg ggt ggc cgc   528
Thr Ile Ala Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg
                165                 170                 175

gtc atg aaa atc aac acc gag gtg cgg agc ttc gga cct gtg tcc cgc   576
Val Met Lys Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg
            180                 185                 190

agc ggc ttc tac ctg gcc ttc cag gac tat ggc ggc tgc atg tcc ctc   624
Ser Gly Phe Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu
        195                 200                 205

atc gcc gtg cgt gtc ttc tac cgc aag tgc ccc cgc atc atc cag aat   672
Ile Ala Val Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn
    210                 215                 220

ggc gcc atc ttc cag gaa acc ctg tcg ggg gct gag agc aca tcg cta   720
Gly Ala Ile Phe Gln Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu
225                 230                 235                 240

gtg gct gcc cgg ggc agc tgc atc gcc aat gcg gaa gag gtg gat gta   768
Val Ala Ala Arg Gly Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val
                245                 250                 255

ccc atc aag ctc tac tgt aac ggg gac ggc gag tgg ctg gtg ccc atc   816
Pro Ile Lys Leu Tyr Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile
            260                 265                 270

ggg cgc tgc atg tgc aaa gca ggc ttc gag gcc gtt gag aat ggc acc   864
Gly Arg Cys Met Cys Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr
        275                 280                 285

gtc tgc cga gag gta cac cct ggt gct aag aag gct gtg aag gtt gaa   912
Val Cys Arg Glu Val His Pro Gly Ala Lys Lys Ala Val Lys Val Glu
    290                 295                 300

gga cct ggg tta aat cac ccc ttc cac tca cta gcg aca gcc tgg agt   960
Gly Pro Gly Leu Asn His Pro Phe His Ser Leu Ala Thr Ala Trp Ser
305                 310                 315                 320

ggg gca tcc acc tgt gct ggg gaa gag gag agg cga gat caa agg atc  1008
Gly Ala Ser Thr Cys Ala Gly Glu Glu Glu Arg Arg Asp Gln Arg Ile
                325                 330                 335
```

```
cca gcc ccc cca tcc act gag tgt gag cgt gca cca tca tgc cca gct   1056
Pro Ala Pro Pro Ser Thr Glu Cys Glu Arg Ala Pro Ser Cys Pro Ala
            340                 345                 350

aat ttt ttg act gct ccc tct tct ggg acc tca ctg gct ccc agg gtc   1104
Asn Phe Leu Thr Ala Pro Ser Ser Gly Thr Ser Leu Ala Pro Arg Val
        355                 360                 365

cca ccc ccc tcc acc tct cgc tct gag ccc ttt gtg gct agt tcc tgt   1152
Pro Pro Pro Ser Thr Ser Arg Ser Glu Pro Phe Val Ala Ser Ser Cys
    370                 375                 380

tca tct ccc gac ctc tcc acc ttg gag ggc ccc agt gct gtg tcc ttg   1200
Ser Ser Pro Asp Leu Ser Thr Leu Glu Gly Pro Ser Ala Val Ser Leu
385                 390                 395                 400

gcc tcc tct tct ctc tcc ctg atg act cca ccc agc ccc aca gct tca   1248
Ala Ser Ser Ser Leu Ser Leu Met Thr Pro Pro Ser Pro Thr Ala Ser
                405                 410                 415

aat gcc ttc tct ggg ctg atc tct agc cca gac ctc tat tct gaa gtg   1296
Asn Ala Phe Ser Gly Leu Ile Ser Ser Pro Asp Leu Tyr Ser Glu Val
            420                 425                 430

tgt gtt tgc atg ggt gcc cac cca ctc aca ggg aaa tca gcc aga gta   1344
Cys Val Cys Met Gly Ala His Pro Leu Thr Gly Lys Ser Ala Arg Val
        435                 440                 445

ttc aga ttc atg tgt aca tct gta tat ttt atc aag cca gat gta cgt   1392
Phe Arg Phe Met Cys Thr Ser Val Tyr Phe Ile Lys Pro Asp Val Arg
    450                 455                 460

gaa aat ggg tac ttg tta gca tat gag gtg gat ttc agg ccc tca ggg   1440
Glu Asn Gly Tyr Leu Leu Ala Tyr Glu Val Asp Phe Arg Pro Ser Gly
465                 470                 475                 480

gaa gca aga tct gga att tct gtg gtg gtg cta ggc aca ttc cat aca   1488
Glu Ala Arg Ser Gly Ile Ser Val Val Val Leu Gly Thr Phe His Thr
                485                 490                 495

cat ctt cac caa tcc ctg gga gca gga gtt gcc cac ccc gtc tta caa   1536
His Leu His Gln Ser Leu Gly Ala Gly Val Ala His Pro Val Leu Gln
            500                 505                 510

gtg aga aaa cag ggc ttg tgc ggt ctc aca gag cac att aat gga act   1584
Val Arg Lys Gln Gly Leu Cys Gly Leu Thr Glu His Ile Asn Gly Thr
        515                 520                 525

gcc ttt tac act cag gac cgc att aga cct ttc cca cca tcc cag gct   1632
Ala Phe Tyr Thr Gln Asp Arg Ile Arg Pro Phe Pro Pro Ser Gln Ala
    530                 535                 540

gcc gcg gcc agt gta gga atg agc tta ttg ggt tgg ctg gtt tgc cga   1680
Ala Ala Ala Ser Val Gly Met Ser Leu Leu Gly Trp Leu Val Cys Arg
545                 550                 555                 560

gat ggt gcc act gca ctc cag cct ggc cgg cag agc aag act gtc aca   1728
Asp Gly Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Lys Thr Val Thr
                565                 570                 575
```

```
aaa aaa aaa gaa aaa gaa aaa gaa aag aaa agc aaa ttc cag gaa agg   1776
Lys Lys Lys Glu Lys Glu Lys Glu Lys Lys Ser Lys Phe Gln Glu Arg
            580                 585                 590

gag ctg gtg gat tgc ttg gcc att gag cct ccc ctt cgt gct gcc ctc   1824
Glu Leu Val Asp Cys Leu Ala Ile Glu Pro Pro Leu Arg Ala Ala Leu
        595                 600                 605

cag gag ctt cac atc cac cta atg aag gaa att ggg ggc ggg gcc tgt   1872
Gln Glu Leu His Ile His Leu Met Lys Glu Ile Gly Gly Gly Ala Cys
    610                 615                 620

gga gag cga gac gtt gcc tgt gaa ggc agg agg gag ggg act tca ggg   1920
Gly Glu Arg Asp Val Ala Cys Glu Gly Arg Arg Glu Gly Thr Ser Gly
625                 630                 635                 640

cag cca gag gga gag gga cgt ggc ccc aca gcc aga agg gcc att cat   1968
Gln Pro Glu Gly Glu Gly Arg Gly Pro Thr Ala Arg Arg Ala Ile His
                645                 650                 655

gtt gag ctg ggt cct ggc ctc agg ctc tct gag cct cag caa ttc aca   2016
Val Glu Leu Gly Pro Gly Leu Arg Leu Ser Glu Pro Gln Gln Phe Thr
            660                 665                 670

ctc tgg gta ttt tgt ctt cct ggg gca ctg ccg gca ggg cta gga tat   2064
Leu Trp Val Phe Cys Leu Pro Gly Ala Leu Pro Ala Gly Leu Gly Tyr
        675                 680                 685

ttc tgc aca aag ggc ctg tgc cac agg agg ttg acc tcg aga tgg gca   2112
Phe Cys Thr Lys Gly Leu Cys His Arg Arg Leu Thr Ser Arg Trp Ala
    690                 695                 700

gct gag gtg ggt gct ggc aga ggc tgt gga ggg gcc atc tgg gag gta   2160
Ala Glu Val Gly Ala Gly Arg Gly Cys Gly Gly Ala Ile Trp Glu Val
705                 710                 715                 720

ggg tca gca gta ggc acc acg agg cat tgg gag atg ggt ggg cat gcc   2208
Gly Ser Ala Val Gly Thr Thr Arg His Trp Glu Met Gly Gly His Ala
                725                 730                 735

cgg att ttc ctg aat gaa gtt ggt ctc cct gcg ccc cct gcc tgc cct   2256
Arg Ile Phe Leu Asn Glu Val Gly Leu Pro Ala Pro Pro Ala Cys Pro
            740                 745                 750

ctt ccc cat cca gcc att ccc ctc tgg cag ctc cag aac cat ctt tct   2304
Leu Pro His Pro Ala Ile Pro Leu Trp Gln Leu Gln Asn His Leu Ser
        755                 760                 765

aaa atg gaa atc tgc atg ccc tca agc ctt gat cat cac tgc gac aac   2352
Lys Met Glu Ile Cys Met Pro Ser Ser Leu Asp His His Cys Asp Asn
    770                 775                 780

cac agc tgc att tct gag tgc cat ctg ggg gac acc atg cca ggc aag   2400
His Ser Cys Ile Ser Glu Cys His Leu Gly Asp Thr Met Pro Gly Lys
785                 790                 795                 800

acc cac tgt ttc tca cgt tgg ctc tgg ctc agt gca ata acg aaa aca   2448
Thr His Cys Phe Ser Arg Trp Leu Trp Leu Ser Ala Ile Thr Lys Thr
                805                 810                 815
```

```
agg gca ata ata atg ggg ttt cac cac gtt ggc cag gct ggt ctc aaa   2496
Arg Ala Ile Ile Met Gly Phe His His Val Gly Gln Ala Gly Leu Lys
            820                 825                 830

ctc ctg gcc tca agt gat ctc ctc acc ttg gcc tcc cta agt gct ggg   2544
Leu Leu Ala Ser Ser Asp Leu Leu Thr Leu Ala Ser Leu Ser Ala Gly
        835                 840                 845

att ata ggt gtg agc cac cga aga gaa agc ata ttc act att cat tca   2592
Ile Ile Gly Val Ser His Arg Arg Glu Ser Ile Phe Thr Ile His Ser
    850                 855                 860

gtg gaa gta gat tgt cat aaa ggt cat cct cct cgt ctt               2631
Val Glu Val Asp Cys His Lys Gly His Pro Pro Arg Leu
865                 870                 875
```

<210> 58
<211> 877
<212> PRT
<213> Homo sapiens

<400> 58

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Val Ala Ser Arg Trp Arg Arg Thr Leu Gly Ala Gln Pro Leu Ser Val
 1               5                  10                  15
Cys Leu Phe Val Cys Phe Val Leu Phe Cys Leu Leu Arg His Ser Leu
            20                  25                  30
Ala Leu Ser Pro Arg Leu Ala Cys Asn Glu Thr Leu Met Asp Ser Thr
        35                  40                  45
Thr Ala Thr Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp
    50                  55                  60
Glu Glu Val Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr
65                  70                  75                  80
Gln Val Cys Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr
                85                  90                  95
Lys Phe Ile Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys
            100                 105                 110
Phe Ser Val Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys
        115                 120                 125
Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala
    130                 135                 140
Thr Lys Thr Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp
145                 150                 155                 160
Thr Ile Ala Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg
                165                 170                 175
Val Met Lys Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg
            180                 185                 190
Ser Gly Phe Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu
        195                 200                 205
Ile Ala Val Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn
    210                 215                 220
Gly Ala Ile Phe Gln Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu
225                 230                 235                 240
Val Ala Ala Arg Gly Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val
                245                 250                 255
Pro Ile Lys Leu Tyr Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile
            260                 265                 270
Gly Arg Cys Met Cys Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr
        275                 280                 285
Val Cys Arg Glu Val His Pro Gly Ala Lys Lys Ala Val Lys Val Glu
    290                 295                 300
```

```
Gly Pro Gly Leu Asn His Pro Phe His Ser Leu Ala Thr Ala Trp Ser
305                 310                 315                 320
Gly Ala Ser Thr Cys Ala Gly Glu Glu Glu Arg Arg Asp Gln Arg Ile
                325                 330                 335
Pro Ala Pro Pro Ser Thr Glu Cys Glu Arg Ala Pro Ser Cys Pro Ala
            340                 345                 350
Asn Phe Leu Thr Ala Pro Ser Ser Gly Thr Ser Leu Ala Pro Arg Val
        355                 360                 365
Pro Pro Pro Ser Thr Ser Arg Ser Glu Pro Phe Val Ala Ser Ser Cys
    370                 375                 380
Ser Ser Pro Asp Leu Ser Thr Leu Glu Gly Pro Ser Ala Val Ser Leu
385                 390                 395                 400
Ala Ser Ser Ser Leu Ser Leu Met Thr Pro Pro Ser Pro Thr Ala Ser
                405                 410                 415
Asn Ala Phe Ser Gly Leu Ile Ser Ser Pro Asp Leu Tyr Ser Glu Val
            420                 425                 430
Cys Val Cys Met Gly Ala His Pro Leu Thr Gly Lys Ser Ala Arg Val
        435                 440                 445
Phe Arg Phe Met Cys Thr Ser Val Tyr Phe Ile Lys Pro Asp Val Arg
    450                 455                 460
Glu Asn Gly Tyr Leu Leu Ala Tyr Glu Val Asp Phe Arg Pro Ser Gly
465                 470                 475                 480
Glu Ala Arg Ser Gly Ile Ser Val Val Val Leu Gly Thr Phe His Thr
                485                 490                 495
His Leu His Gln Ser Leu Gly Ala Gly Val Ala His Pro Val Leu Gln
            500                 505                 510
Val Arg Lys Gln Gly Leu Cys Gly Leu Thr Glu His Ile Asn Gly Thr
        515                 520                 525
Ala Phe Tyr Thr Gln Asp Arg Ile Arg Pro Phe Pro Pro Ser Gln Ala
    530                 535                 540
Ala Ala Ala Ser Val Gly Met Ser Leu Leu Gly Trp Leu Val Cys Arg
545                 550                 555                 560
Asp Gly Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Lys Thr Val Thr
                565                 570                 575
Lys Lys Lys Glu Lys Glu Lys Glu Lys Lys Ser Lys Phe Gln Glu Arg
            580                 585                 590
Glu Leu Val Asp Cys Leu Ala Ile Glu Pro Pro Leu Arg Ala Ala Leu
        595                 600                 605
Gln Glu Leu His Ile His Leu Met Lys Glu Ile Gly Gly Gly Ala Cys
    610                 615                 620
Gly Glu Arg Asp Val Ala Cys Glu Gly Arg Arg Glu Gly Thr Ser Gly
625                 630                 635                 640
Gln Pro Glu Gly Glu Gly Arg Gly Pro Thr Ala Arg Arg Ala Ile His
                645                 650                 655
Val Glu Leu Gly Pro Gly Leu Arg Leu Ser Glu Pro Gln Gln Phe Thr
            660                 665                 670
Leu Trp Val Phe Cys Leu Pro Gly Ala Leu Pro Ala Gly Leu Gly Tyr
        675                 680                 685
Phe Cys Thr Lys Gly Leu Cys His Arg Arg Leu Thr Ser Arg Trp Ala
    690                 695                 700
Ala Glu Val Gly Ala Gly Arg Gly Cys Gly Gly Ala Ile Trp Glu Val
705                 710                 715                 720
Gly Ser Ala Val Gly Thr Thr Arg His Trp Glu Met Gly Gly His Ala
                725                 730                 735
Arg Ile Phe Leu Asn Glu Val Gly Leu Pro Ala Pro Pro Ala Cys Pro
            740                 745                 750
Leu Pro His Pro Ala Ile Pro Leu Trp Gln Leu Gln Asn His Leu Ser
        755                 760                 765
Lys Met Glu Ile Cys Met Pro Ser Ser Leu Asp His His Cys Asp Asn
    770                 775                 780
His Ser Cys Ile Ser Glu Cys His Leu Gly Asp Thr Met Pro Gly Lys
785                 790                 795                 800
```

```
Thr His Cys Phe Ser Arg Trp Leu Trp Leu Ser Ala Ile Thr Lys Thr
                805                 810                 815
Arg Ala Ile Ile Met Gly Phe His His Val Gly Gln Ala Gly Leu Lys
            820                 825                 830
Leu Leu Ala Ser Ser Asp Leu Leu Thr Leu Ala Ser Leu Ser Ala Gly
        835                 840                 845
Ile Ile Gly Val Ser His Arg Arg Glu Ser Ile Phe Thr Ile His Ser
    850                 855                 860
Val Glu Val Asp Cys His Lys Gly His Pro Pro Arg Leu
865                 870                 875


<210> 59
<211> 3930
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(3930)
<223> MOOSE03639

<400> 59
atg gca gtg cct agt ctg tgg ccc tgg gga gca tgc ctg cct gtg atc   48
Met Ala Val Pro Ser Leu Trp Pro Trp Gly Ala Cys Leu Pro Val Ile
 1               5                  10                  15

ttc ctc tcc ttg gga ttt ggc ctg gat aca gta gag gtg tgc ccc agc   96
Phe Leu Ser Leu Gly Phe Gly Leu Asp Thr Val Glu Val Cys Pro Ser
            20                  25                  30

ctg gat att cgc tca gag gtg gca gag ctt cgt cag ctg gag aac tgc   144
Leu Asp Ile Arg Ser Glu Val Ala Glu Leu Arg Gln Leu Glu Asn Cys
        35                  40                  45

agc gtg gtg gag ggc cac ctg cag atc ctg ctc atg ttc aca gcc acc   192
Ser Val Val Glu Gly His Leu Gln Ile Leu Leu Met Phe Thr Ala Thr
    50                  55                  60

ggg gag gac ttc cgc ggc ctc agc ttc cct cgc ctc acc cag gtc acc   240
Gly Glu Asp Phe Arg Gly Leu Ser Phe Pro Arg Leu Thr Gln Val Thr
65                  70                  75                  80

gac tac ctg ctg ctc ttc cgt gtc tac gga ctg gag agc ctg cgc gac   288
Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu Glu Ser Leu Arg Asp
                85                  90                  95

ctc ttc ccc aac cta gca gtc atc cgc ggg acg cgc ctc ttc ctg ggc   336
Leu Phe Pro Asn Leu Ala Val Ile Arg Gly Thr Arg Leu Phe Leu Gly
            100                 105                 110

tat gca ctg gtc atc ttt gag atg cca cat ctg cgt gac gtg gca ctg   384
Tyr Ala Leu Val Ile Phe Glu Met Pro His Leu Arg Asp Val Ala Leu
        115                 120                 125

cct gca ctt ggg gcc gtg ctg cgt ggg gct gtg cgt gtg gag aag aac   432
Pro Ala Leu Gly Ala Val Leu Arg Gly Ala Val Arg Val Glu Lys Asn
    130                 135                 140

cag gag ctc tgc cac ctc tcc acc att gac tgg gga ctg ctg cag cca   480
Gln Glu Leu Cys His Leu Ser Thr Ile Asp Trp Gly Leu Leu Gln Pro
145                 150                 155                 160
```

```
gca cct ggc gcc aac cac atc gtg ggc aac aag ctg ggc gag gag tgt   528
Ala Pro Gly Ala Asn His Ile Val Gly Asn Lys Leu Gly Glu Glu Cys
                165                 170                 175

gct gac gtg tgc cct ggt gtg ctg ggt gct gct ggt gag ccc tgt gcc   576
Ala Asp Val Cys Pro Gly Val Leu Gly Ala Ala Gly Glu Pro Cys Ala
            180                 185                 190

aag acc acc ttc agc ggg cac act gac tac aga tgc tgg acc tcc agc   624
Lys Thr Thr Phe Ser Gly His Thr Asp Tyr Arg Cys Trp Thr Ser Ser
        195                 200                 205

cac tgc cag aga gtg tgc ccc tgc ccc cat ggg atg gct tgc aca gcg   672
His Cys Gln Arg Val Cys Pro Cys Pro His Gly Met Ala Cys Thr Ala
    210                 215                 220

agg ggc gag tgc tgc cac acc gaa tgc ctg ggg ggc tgc agc cag cca   720
Arg Gly Glu Cys Cys His Thr Glu Cys Leu Gly Gly Cys Ser Gln Pro
225                 230                 235                 240

gaa gac cct cgt gcc tgt gta gct tgc cgc cac ctc tac ttc cag ggt   768
Glu Asp Pro Arg Ala Cys Val Ala Cys Arg His Leu Tyr Phe Gln Gly
                245                 250                 255

gcc tgc ctg tgg gcc tgc ccg cca ggc acc tac cag tat gag tcc tgg   816
Ala Cys Leu Trp Ala Cys Pro Pro Gly Thr Tyr Gln Tyr Glu Ser Trp
            260                 265                 270

cgc tgt gtc aca gct gag cgc tgt gcc agc ctg cac tct gtg ccc ggc   864
Arg Cys Val Thr Ala Glu Arg Cys Ala Ser Leu His Ser Val Pro Gly
        275                 280                 285

cgt gcc tcc acc ttc ggc ata cac cag ggc agt tgc ctg gcc cag tgc   912
Arg Ala Ser Thr Phe Gly Ile His Gln Gly Ser Cys Leu Ala Gln Cys
    290                 295                 300

cct tct ggc ttc acc cgt aat agc agc agc ata ttc tgc cac aag tgc   960
Pro Ser Gly Phe Thr Arg Asn Ser Ser Ser Ile Phe Cys His Lys Cys
305                 310                 315                 320

gag ggg ctg tgc cct aaa gag tgc aag gta ggc acc aag acc atc gac   1008
Glu Gly Leu Cys Pro Lys Glu Cys Lys Val Gly Thr Lys Thr Ile Asp
                325                 330                 335

tcc atc cag gcg gca cag gat ctt gtg ggc tgc acg cat gtg gag gga   1056
Ser Ile Gln Ala Ala Gln Asp Leu Val Gly Cys Thr His Val Glu Gly
            340                 345                 350

agc ctc atc ctc aac ctt cgc cag ggc tac aac ctg gag cca cag ctg   1104
Ser Leu Ile Leu Asn Leu Arg Gln Gly Tyr Asn Leu Glu Pro Gln Leu
        355                 360                 365

cag cac agc ctg ggg ctg gta gaa acc att act ggc ttc ctc aaa atc   1152
Gln His Ser Leu Gly Leu Val Glu Thr Ile Thr Gly Phe Leu Lys Ile
    370                 375                 380

aag cac tcc ttt gcc ctc gtg tcc ctg ggc ttt ttc aag aac ctc aaa   1200
Lys His Ser Phe Ala Leu Val Ser Leu Gly Phe Phe Lys Asn Leu Lys
385                 390                 395                 400
```

```
cta atc cgg gga gac gcc atg gtg gat ggg aac tac act ctc tac gtg   1248
Leu Ile Arg Gly Asp Ala Met Val Asp Gly Asn Tyr Thr Leu Tyr Val
                405                 410                 415

ctg gac aac cag aac cta caa cag cta ggg tcc tgg gtg gcc gcg ggg   1296
Leu Asp Asn Gln Asn Leu Gln Gln Leu Gly Ser Trp Val Ala Ala Gly
            420                 425                 430

ctc acc att ccc gtg ggc aag atc tac ttc gcc ttc aac ccg cgc ctc   1344
Leu Thr Ile Pro Val Gly Lys Ile Tyr Phe Ala Phe Asn Pro Arg Leu
        435                 440                 445

tgc ttg gaa cac atc tac cga ctg gag gag gtg aca ggc acg cga ggt   1392
Cys Leu Glu His Ile Tyr Arg Leu Glu Glu Val Thr Gly Thr Arg Gly
    450                 455                 460

cgg cag aac aag gct gag atc aac ccc cgc acc aac gga gac cgc gcc   1440
Arg Gln Asn Lys Ala Glu Ile Asn Pro Arg Thr Asn Gly Asp Arg Ala
465                 470                 475                 480

gcc tgc cag act cgc acc ctg cgc ttc gtg tcc aac gtg acg gag gca   1488
Ala Cys Gln Thr Arg Thr Leu Arg Phe Val Ser Asn Val Thr Glu Ala
                485                 490                 495

gac cgc atc ctg cta cgc tgg gag cgc tat gag cca ctg gag gcc cgc   1536
Asp Arg Ile Leu Leu Arg Trp Glu Arg Tyr Glu Pro Leu Glu Ala Arg
            500                 505                 510

gac ctg ctc agc ttc atc gtg tac tac aag gag tcc cca ttc cag aac   1584
Asp Leu Leu Ser Phe Ile Val Tyr Tyr Lys Glu Ser Pro Phe Gln Asn
        515                 520                 525

gcc aca gag cac gtg ggt cca gat gct tgt gga acc cag agc tgg aac   1632
Ala Thr Glu His Val Gly Pro Asp Ala Cys Gly Thr Gln Ser Trp Asn
    530                 535                 540

ctg ctg gat gtg gag ctg ccc cta agc cgc acc cag gag cca ggg gtg   1680
Leu Leu Asp Val Glu Leu Pro Leu Ser Arg Thr Gln Glu Pro Gly Val
545                 550                 555                 560

acc cta gcc tcc ctc aag cct tgg aca cag tac gca gtg ttt gtg cgg   1728
Thr Leu Ala Ser Leu Lys Pro Trp Thr Gln Tyr Ala Val Phe Val Arg
                565                 570                 575

gcc atc acg cta acc act gag gag gac agc cct cat caa gga gcc cag   1776
Ala Ile Thr Leu Thr Thr Glu Glu Asp Ser Pro His Gln Gly Ala Gln
            580                 585                 590

agt ccc atc gtc tac ctc cga acg ctg cct gca gct ccc acg gtg ccc   1824
Ser Pro Ile Val Tyr Leu Arg Thr Leu Pro Ala Ala Pro Thr Val Pro
        595                 600                 605

caa gac gtc atc tcc acg tcc aac tcc tcc tcc cac ctc ctg gtg cgc   1872
Gln Asp Val Ile Ser Thr Ser Asn Ser Ser Ser His Leu Leu Val Arg
    610                 615                 620

tgg aag cca ccg acc cag cgc aat ggg aac ctc acc tac tac ctg gtg   1920
Trp Lys Pro Pro Thr Gln Arg Asn Gly Asn Leu Thr Tyr Tyr Leu Val
625                 630                 635                 640
```

```
ctg tgg cag cgg ctg gca gag gac ggc gac ctc tac ctc aat gac tac   1968
Leu Trp Gln Arg Leu Ala Glu Asp Gly Asp Leu Tyr Leu Asn Asp Tyr
                645                 650                 655

tgc cac cgc ggc ttg cgg ctg ccc acc agc aac aac gat ccg cgc ttc   2016
Cys His Arg Gly Leu Arg Leu Pro Thr Ser Asn Asn Asp Pro Arg Phe
            660                 665                 670

gac ggc gaa gac ggg gat cct gag gcc gag atg gag tcc gac tgc tgc   2064
Asp Gly Glu Asp Gly Asp Pro Glu Ala Glu Met Glu Ser Asp Cys Cys
        675                 680                 685

cct tgc cag cac cca cct cct ggt cag gtt ctg ccc ccg ctg gag gcg   2112
Pro Cys Gln His Pro Pro Pro Gly Gln Val Leu Pro Pro Leu Glu Ala
    690                 695                 700

caa gag gcc tcg ttc cag aag aag ttt gaa aac ttt cta cac aac gcg   2160
Gln Glu Ala Ser Phe Gln Lys Lys Phe Glu Asn Phe Leu His Asn Ala
705                 710                 715                 720

atc acc atc ccc ata tcc cct tgg aag gtg acg tcc atc aac aag agc   2208
Ile Thr Ile Pro Ile Ser Pro Trp Lys Val Thr Ser Ile Asn Lys Ser
                725                 730                 735

ccc caa agg gac tca ggg cgg cac cgc cgg gca gct ggg ccc ctc cgg   2256
Pro Gln Arg Asp Ser Gly Arg His Arg Arg Ala Ala Gly Pro Leu Arg
            740                 745                 750

ctg ggg ggc aac agc tcg gat ttc gag atc cag gag gac aag gtg ccc   2304
Leu Gly Gly Asn Ser Ser Asp Phe Glu Ile Gln Glu Asp Lys Val Pro
        755                 760                 765

cgt gag cga gcg gtg ctg agc ggc ctg cgc cac ttc acg gaa tac cgg   2352
Arg Glu Arg Ala Val Leu Ser Gly Leu Arg His Phe Thr Glu Tyr Arg
    770                 775                 780

atc gac atc cat gcc tgc aac cac gcg gcg cac acc gtg ggc tgc agc   2400
Ile Asp Ile His Ala Cys Asn His Ala Ala His Thr Val Gly Cys Ser
785                 790                 795                 800

gcc gcc acc ttc gtc ttt gcg cgc acc atg ccc cac aga gag gct gat   2448
Ala Ala Thr Phe Val Phe Ala Arg Thr Met Pro His Arg Glu Ala Asp
                805                 810                 815

ggt att cca gga aag gtg gcc tgg gag gcc tcc agc aag aac agt gtc   2496
Gly Ile Pro Gly Lys Val Ala Trp Glu Ala Ser Ser Lys Asn Ser Val
            820                 825                 830

ctt ctg cgc tgg ctc gag cca cca gac ccc aac gga ctc atc ctc aag   2544
Leu Leu Arg Trp Leu Glu Pro Pro Asp Pro Asn Gly Leu Ile Leu Lys
        835                 840                 845

tac gaa atc aag tac cgc cgc ttg gga gag gag gcc aca gtg ctg tgt   2592
Tyr Glu Ile Lys Tyr Arg Arg Leu Gly Glu Glu Ala Thr Val Leu Cys
    850                 855                 860

gtg tcc cgt ctt cga tat gcg aag ttt ggg gga gtc cac ctg gcc ctg   2640
Val Ser Arg Leu Arg Tyr Ala Lys Phe Gly Gly Val His Leu Ala Leu
865                 870                 875                 880
```

```
ctg ccc cct gga aac tac tct gcc agg gtt agg gca acc tca ctg gct   2688
Leu Pro Pro Gly Asn Tyr Ser Ala Arg Val Arg Ala Thr Ser Leu Ala
                885                 890                 895

ggc aat ggc tct tgg aca gac agt gtt gcc ttc tac atc ctt ggc cca   2736
Gly Asn Gly Ser Trp Thr Asp Ser Val Ala Phe Tyr Ile Leu Gly Pro
            900                 905                 910

gag gag gag gat gct ggg ggg ctg cat gtc ctc ctc act gcc acc cct   2784
Glu Glu Glu Asp Ala Gly Gly Leu His Val Leu Leu Thr Ala Thr Pro
        915                 920                 925

gtg ggg ctc acg ctg ctc atc gtt ctt gct gcc ctt ggt ttc ttc tac   2832
Val Gly Leu Thr Leu Leu Ile Val Leu Ala Ala Leu Gly Phe Phe Tyr
    930                 935                 940

ggc aag aag aga aac aga acc ctg tat gct tct gtg aat cca gag tac   2880
Gly Lys Lys Arg Asn Arg Thr Leu Tyr Ala Ser Val Asn Pro Glu Tyr
945                 950                 955                 960

ttc agc gcc tct gat agt agg tct ggg atg tat gtc cct gat gaa tgg   2928
Phe Ser Ala Ser Asp Ser Arg Ser Gly Met Tyr Val Pro Asp Glu Trp
                965                 970                 975

gag gtg cct cgg gag cag atc tcg ata atc cgg gaa ctg ggc cag ggc   2976
Glu Val Pro Arg Glu Gln Ile Ser Ile Ile Arg Glu Leu Gly Gln Gly
            980                 985                 990

tct ttt ggg atg gta tat gag ggg ctg gca cga gga ctt gag gct gga   3024
Ser Phe Gly Met Val Tyr Glu Gly Leu Ala Arg Gly Leu Glu Ala Gly
        995                 1000                1005

gag gag tcc aca ccc gtg gcc ctg aag acg gtg aat gag ctg gcc agc   3072
Glu Glu Ser Thr Pro Val Ala Leu Lys Thr Val Asn Glu Leu Ala Ser
    1010                1015                1020

cca cgg gaa tgc att gag ttc ctc aag gaa gct tct gtc atg aaa gcc   3120
Pro Arg Glu Cys Ile Glu Phe Leu Lys Glu Ala Ser Val Met Lys Ala
1025                1030                1035                1040

ttc aag tgt cac cat gtg gtg cgt ctc ctg ggt gtg gta tct cag ggc   3168
Phe Lys Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
                1045                1050                1055

cag cca act ctg gtc atc atg gag tta atg acc cgt ggg gac ctc aag   3216
Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
            1060                1065                1070

agc cat ctt cga tct ttg cgg cct gag gca gag aac aac cct ggg ctc   3264
Ser His Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly Leu
        1075                1080                1085

cca cag cca gca ttg ggg gaa atg atc caa atg gct ggt gag att gca   3312
Pro Gln Pro Ala Leu Gly Glu Met Ile Gln Met Ala Gly Glu Ile Ala
    1090                1095                1100

gac ggc atg gcc tac ctt gct gcc aac aag ttt gtg cac cga gat cta   3360
Asp Gly Met Ala Tyr Leu Ala Ala Asn Lys Phe Val His Arg Asp Leu
1105                1110                1115                1120
```

```
gca gcc cgc aac tgc atg gtg tcc cag gac ttc acc gtc aag atc ggg   3408
Ala Ala Arg Asn Cys Met Val Ser Gln Asp Phe Thr Val Lys Ile Gly
                1125                1130                1135

gac ttc ggg atg act cgg gac gtg tat gag aca gac tat tac cgc aag   3456
Asp Phe Gly Met Thr Arg Asp Val Tyr Glu Thr Asp Tyr Tyr Arg Lys
            1140                1145                1150

ggt ggg aag ggg ctg ctg ccc gtg cgc tgg atg gcc ccc gag tcc ctc   3504
Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu
        1155                1160                1165

aaa gat ggg atc ttc acc acc cac tcg gat gtc tgg tcc ttt ggc gtg   3552
Lys Asp Gly Ile Phe Thr Thr His Ser Asp Val Trp Ser Phe Gly Val
    1170                1175                1180

gta ctc tgg gag att gtg acc ctg gca gaa caa ccc tac cag ggc ctg   3600
Val Leu Trp Glu Ile Val Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
1185                1190                1195                1200

tcc aat gag cag gtg ctg aag ttc gtc atg gat ggc ggg gtc ctg gag   3648
Ser Asn Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Val Leu Glu
                1205                1210                1215

gag ctg gag ggc tgt ccc ctt cag ctg cag gag ctg atg agc cgc tgc   3696
Glu Leu Glu Gly Cys Pro Leu Gln Leu Gln Glu Leu Met Ser Arg Cys
            1220                1225                1230

tgg cag ccg aac cca cgc ctg cgc cca tct ttc aca cac att ctg gac   3744
Trp Gln Pro Asn Pro Arg Leu Arg Pro Ser Phe Thr His Ile Leu Asp
        1235                1240                1245

agc ata cag gag gag ctg cgg ccc tcc ttc cgc ctc ctc tcc ttc tac   3792
Ser Ile Gln Glu Glu Leu Arg Pro Ser Phe Arg Leu Leu Ser Phe Tyr
    1250                1255                1260

tac agc ccg gaa tgc cgg ggg gcc cgg ggc tcc ctg cct acc acc gat   3840
Tyr Ser Pro Glu Cys Arg Gly Ala Arg Gly Ser Leu Pro Thr Thr Asp
1265                1270                1275                1280

gca gag cct gac tcc tca ccc act cca aga gac tgc agc cct caa aat   3888
Ala Glu Pro Asp Ser Ser Pro Thr Pro Arg Asp Cys Ser Pro Gln Asn
                1285                1290                1295

ggg gga ggc aga ggt tgc aga gag ccg aga tcg cac cat tgc           3930
Gly Gly Gly Arg Gly Cys Arg Glu Pro Arg Ser His His Cys
            1300                1305                1310
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<210> 60
<211> 1310
<212> PRT
<213> Homo sapiens

<400> 60

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Met Ala Val Pro Ser Leu Trp Pro Trp Gly Ala Cys Leu Pro Val Ile
 1               5                  10                  15
Phe Leu Ser Leu Gly Phe Gly Leu Asp Thr Val Glu Val Cys Pro Ser
            20                  25                  30
Leu Asp Ile Arg Ser Glu Val Ala Glu Leu Arg Gln Leu Glu Asn Cys
        35                  40                  45
```

```
Ser Val Val Glu Gly His Leu Gln Ile Leu Leu Met Phe Thr Ala Thr
    50                  55                  60
Gly Glu Asp Phe Arg Gly Leu Ser Phe Pro Arg Leu Thr Gln Val Thr
65                  70                  75                  80
Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu Glu Ser Leu Arg Asp
                85                  90                  95
Leu Phe Pro Asn Leu Ala Val Ile Arg Gly Thr Arg Leu Phe Leu Gly
            100                 105                 110
Tyr Ala Leu Val Ile Phe Glu Met Pro His Leu Arg Asp Val Ala Leu
        115                 120                 125
Pro Ala Leu Gly Ala Val Leu Arg Gly Ala Val Arg Val Glu Lys Asn
    130                 135                 140
Gln Glu Leu Cys His Leu Ser Thr Ile Asp Trp Gly Leu Leu Gln Pro
145                 150                 155                 160
Ala Pro Gly Ala Asn His Ile Val Gly Asn Lys Leu Gly Glu Glu Cys
                165                 170                 175
Ala Asp Val Cys Pro Gly Val Leu Gly Ala Ala Gly Glu Pro Cys Ala
            180                 185                 190
Lys Thr Thr Phe Ser Gly His Thr Asp Tyr Arg Cys Trp Thr Ser Ser
        195                 200                 205
His Cys Gln Arg Val Cys Pro Cys Pro His Gly Met Ala Cys Thr Ala
    210                 215                 220
Arg Gly Glu Cys Cys His Thr Glu Cys Leu Gly Gly Cys Ser Gln Pro
225                 230                 235                 240
Glu Asp Pro Arg Ala Cys Val Ala Cys Arg His Leu Tyr Phe Gln Gly
                245                 250                 255
Ala Cys Leu Trp Ala Cys Pro Pro Gly Thr Tyr Gln Tyr Glu Ser Trp
            260                 265                 270
Arg Cys Val Thr Ala Glu Arg Cys Ala Ser Leu His Ser Val Pro Gly
        275                 280                 285
Arg Ala Ser Thr Phe Gly Ile His Gln Gly Ser Cys Leu Ala Gln Cys
    290                 295                 300
Pro Ser Gly Phe Thr Arg Asn Ser Ser Ser Ile Phe Cys His Lys Cys
305                 310                 315                 320
Glu Gly Leu Cys Pro Lys Glu Cys Lys Val Gly Thr Lys Thr Ile Asp
                325                 330                 335
Ser Ile Gln Ala Ala Gln Asp Leu Val Gly Cys Thr His Val Glu Gly
            340                 345                 350
Ser Leu Ile Leu Asn Leu Arg Gln Gly Tyr Asn Leu Glu Pro Gln Leu
        355                 360                 365
Gln His Ser Leu Gly Leu Val Glu Thr Ile Thr Gly Phe Leu Lys Ile
    370                 375                 380
Lys His Ser Phe Ala Leu Val Ser Leu Gly Phe Phe Lys Asn Leu Lys
385                 390                 395                 400
Leu Ile Arg Gly Asp Ala Met Val Asp Gly Asn Tyr Thr Leu Tyr Val
                405                 410                 415
Leu Asp Asn Gln Asn Leu Gln Gln Leu Gly Ser Trp Val Ala Ala Gly
            420                 425                 430
Leu Thr Ile Pro Val Gly Lys Ile Tyr Phe Ala Phe Asn Pro Arg Leu
        435                 440                 445
Cys Leu Glu His Ile Tyr Arg Leu Glu Glu Val Thr Gly Thr Arg Gly
    450                 455                 460
Arg Gln Asn Lys Ala Glu Ile Asn Pro Arg Thr Asn Gly Asp Arg Ala
465                 470                 475                 480
Ala Cys Gln Thr Arg Thr Leu Arg Phe Val Ser Asn Val Thr Glu Ala
                485                 490                 495
Asp Arg Ile Leu Leu Arg Trp Glu Arg Tyr Glu Pro Leu Glu Ala Arg
            500                 505                 510
Asp Leu Leu Ser Phe Ile Val Tyr Tyr Lys Glu Ser Pro Phe Gln Asn
        515                 520                 525
Ala Thr Glu His Val Gly Pro Asp Ala Cys Gly Thr Gln Ser Trp Asn
    530                 535                 540
```

```
Leu Leu Asp Val Glu Leu Pro Leu Ser Arg Thr Gln Glu Pro Gly Val
545                 550                 555                 560
Thr Leu Ala Ser Leu Lys Pro Trp Thr Gln Tyr Ala Val Phe Val Arg
                565                 570                 575
Ala Ile Thr Leu Thr Thr Glu Glu Asp Ser Pro His Gln Gly Ala Gln
            580                 585                 590
Ser Pro Ile Val Tyr Leu Arg Thr Leu Pro Ala Ala Pro Thr Val Pro
        595                 600                 605
Gln Asp Val Ile Ser Thr Ser Asn Ser Ser Ser His Leu Leu Val Arg
    610                 615                 620
Trp Lys Pro Pro Thr Gln Arg Asn Gly Asn Leu Thr Tyr Tyr Leu Val
625                 630                 635                 640
Leu Trp Gln Arg Leu Ala Glu Asp Gly Asp Leu Tyr Leu Asn Asp Tyr
                645                 650                 655
Cys His Arg Gly Leu Arg Leu Pro Thr Ser Asn Asn Asp Pro Arg Phe
            660                 665                 670
Asp Gly Glu Asp Gly Asp Pro Glu Ala Glu Met Glu Ser Asp Cys Cys
        675                 680                 685
Pro Cys Gln His Pro Pro Pro Gly Gln Val Leu Pro Pro Leu Glu Ala
    690                 695                 700
Gln Glu Ala Ser Phe Gln Lys Lys Phe Glu Asn Phe Leu His Asn Ala
705                 710                 715                 720
Ile Thr Ile Pro Ile Ser Pro Trp Lys Val Thr Ser Ile Asn Lys Ser
                725                 730                 735
Pro Gln Arg Asp Ser Gly Arg His Arg Arg Ala Ala Gly Pro Leu Arg
            740                 745                 750
Leu Gly Gly Asn Ser Ser Asp Phe Glu Ile Gln Glu Asp Lys Val Pro
        755                 760                 765
Arg Glu Arg Ala Val Leu Ser Gly Leu Arg His Phe Thr Glu Tyr Arg
    770                 775                 780
Ile Asp Ile His Ala Cys Asn His Ala Ala His Thr Val Gly Cys Ser
785                 790                 795                 800
Ala Ala Thr Phe Val Phe Ala Arg Thr Met Pro His Arg Glu Ala Asp
                805                 810                 815
Gly Ile Pro Gly Lys Val Ala Trp Glu Ala Ser Ser Lys Asn Ser Val
            820                 825                 830
Leu Leu Arg Trp Leu Glu Pro Pro Asp Pro Asn Gly Leu Ile Leu Lys
        835                 840                 845
Tyr Glu Ile Lys Tyr Arg Arg Leu Gly Glu Glu Ala Thr Val Leu Cys
    850                 855                 860
Val Ser Arg Leu Arg Tyr Ala Lys Phe Gly Gly Val His Leu Ala Leu
865                 870                 875                 880
Leu Pro Pro Gly Asn Tyr Ser Ala Arg Val Arg Ala Thr Ser Leu Ala
                885                 890                 895
Gly Asn Gly Ser Trp Thr Asp Ser Val Ala Phe Tyr Ile Leu Gly Pro
            900                 905                 910
Glu Glu Glu Asp Ala Gly Gly Leu His Val Leu Leu Thr Ala Thr Pro
        915                 920                 925
Val Gly Leu Thr Leu Leu Ile Val Leu Ala Ala Leu Gly Phe Phe Tyr
    930                 935                 940
Gly Lys Lys Arg Asn Arg Thr Leu Tyr Ala Ser Val Asn Pro Glu Tyr
945                 950                 955                 960
Phe Ser Ala Ser Asp Ser Arg Ser Gly Met Tyr Val Pro Asp Glu Trp
                965                 970                 975
Glu Val Pro Arg Glu Gln Ile Ser Ile Ile Arg Glu Leu Gly Gln Gly
            980                 985                 990
Ser Phe Gly Met Val Tyr Glu Gly Leu Ala Arg Gly Leu Glu Ala Gly
        995                 1000                1005
Glu Glu Ser Thr Pro Val Ala Leu Lys Thr Val Asn Glu Leu Ala Ser
    1010                1015                1020
Pro Arg Glu Cys Ile Glu Phe Leu Lys Glu Ala Ser Val Met Lys Ala
1025                1030                1035                1040
```

```
Phe Lys Cys His His Val Val Arg Leu Leu Gly Val Val Ser Gln Gly
                1045                1050                1055
Gln Pro Thr Leu Val Ile Met Glu Leu Met Thr Arg Gly Asp Leu Lys
            1060                1065                1070
Ser His Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly Leu
        1075                1080                1085
Pro Gln Pro Ala Leu Gly Glu Met Ile Gln Met Ala Gly Glu Ile Ala
    1090                1095                1100
Asp Gly Met Ala Tyr Leu Ala Ala Asn Lys Phe Val His Arg Asp Leu
1105                1110                1115                1120
Ala Ala Arg Asn Cys Met Val Ser Gln Asp Phe Thr Val Lys Ile Gly
                1125                1130                1135
Asp Phe Gly Met Thr Arg Asp Val Tyr Glu Thr Asp Tyr Tyr Arg Lys
            1140                1145                1150
Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu
        1155                1160                1165
Lys Asp Gly Ile Phe Thr Thr His Ser Asp Val Trp Ser Phe Gly Val
    1170                1175                1180
Val Leu Trp Glu Ile Val Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu
1185                1190                1195                1200
Ser Asn Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Val Leu Glu
                1205                1210                1215
Glu Leu Glu Gly Cys Pro Leu Gln Leu Gln Glu Leu Met Ser Arg Cys
            1220                1225                1230
Trp Gln Pro Asn Pro Arg Leu Arg Pro Ser Phe Thr His Ile Leu Asp
        1235                1240                1245
Ser Ile Gln Glu Glu Leu Arg Pro Ser Phe Arg Leu Leu Ser Phe Tyr
    1250                1255                1260
Tyr Ser Pro Glu Cys Arg Gly Ala Arg Gly Ser Leu Pro Thr Thr Asp
1265                1270                1275                1280
Ala Glu Pro Asp Ser Ser Pro Thr Pro Arg Asp Cys Ser Pro Gln Asn
                1285                1290                1295
Gly Gly Gly Arg Gly Cys Arg Glu Pro Arg Ser His His Cys
            1300                1305                1310
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<210> 61
<211> 1455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1455)
<223> MOOSE08717

<400> 61

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atg aat gta atg cat gtg gga aat cct tct gcc aca gat cag ccc tca   48
Met Asn Val Met His Val Gly Asn Pro Ser Ala Thr Asp Gln Pro Ser
 1               5                  10                  15

ctg tgc atc aga gaa cac aca cag ggg aga aac cat aga caa cgg aaa   96
Leu Cys Ile Arg Glu His Thr Gln Gly Arg Asn His Arg Gln Arg Lys
             20                  25                  30

atg tta gca aag cgg aaa cct cct gcc atg ggt cag gac cct cct gca   144
Met Leu Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Asp Pro Pro Ala
         35                  40                  45

acc agt gag cag aaa cag tgg aaa agc agg acc aat gga gct gaa aat   192
Thr Ser Glu Gln Lys Gln Trp Lys Ser Arg Thr Asn Gly Ala Glu Asn
     50                  55                  60
```

```
aaa acg tta aca tta gca gaa tac cat gaa caa gaa gaa atc ttc aaa   240
Lys Thr Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys
 65                  70                  75                  80

ctc cgg tta ggt cat ctt aaa aag gag gaa gca gag atc cag gca gag   288
Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu
                85                  90                  95

ctg gaa agg cta gaa agg gtt aga aat cta cgt atc ggg gaa cta aaa   336
Leu Glu Arg Leu Glu Arg Val Arg Asn Leu Arg Ile Gly Glu Leu Lys
            100                 105                 110

agg ata cat aat gaa gat aac tca caa ttt aaa gat cat cca atg cta   384
Arg Ile His Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro Met Leu
        115                 120                 125

aat gac aga tat ttg ttg tta cat ctt ttg gat aga gga ggt ttc agt   432
Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Asp Arg Gly Gly Phe Ser
    130                 135                 140

aaa gtt tac aag gca ttt gaa cta ata gag caa aga tac gta gct gtg   480
Lys Val Tyr Lys Ala Phe Glu Leu Ile Glu Gln Arg Tyr Val Ala Val
145                 150                 155                 160

aaa att cac cag tta aat aaa aac tgg aga gat gag aaa aag gag aat   528
Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn
                165                 170                 175

tac cac aag cat gca tgt agg gaa tac tgg att cat aaa gaa ctg gat   576
Tyr His Lys His Ala Cys Arg Glu Tyr Trp Ile His Lys Glu Leu Asp
            180                 185                 190

cat ccc aga ata att aag ctg tat gat tac ttt tca ctg gat act gac   624
His Pro Arg Ile Ile Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp
        195                 200                 205

tca ttt tgt aca gtg tta gaa tac tgt gag gga aat gat cta aac ttc   672
Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asn Phe
    210                 215                 220

tat ctg aaa cgg cac aaa tta atg tca gag aaa gag gcc tgg tcc att   720
Tyr Leu Lys Arg His Lys Leu Met Ser Glu Lys Glu Ala Trp Ser Ile
225                 230                 235                 240

atc atg cag act gta aat gct tta aag tac tta aat aaa ata aaa cct   768
Ile Met Gln Thr Val Asn Ala Leu Lys Tyr Leu Asn Lys Ile Lys Pro
                245                 250                 255

ccc atc ata cac tat gac ctc aaa cca ggg aat att ctt tta gta aat   816
Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn
            260                 265                 270

ggt aca gtg tgt gga gag aga aaa att aca gag ctt ggt ctt tcg aag   864
Gly Thr Val Cys Gly Glu Arg Lys Ile Thr Glu Leu Gly Leu Ser Lys
        275                 280                 285

atc atg gat gat gat agc tac aat tca gtg ggt ggc atg gag ctg aca   912
Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Gly Gly Met Glu Leu Thr
    290                 295                 300
```

```
tca caa ggt gct ggc act tat tgc aat tta aca cca gag agt ttt gtg   960
Ser Gln Gly Ala Gly Thr Tyr Cys Asn Leu Thr Pro Glu Ser Phe Val
305                 310                 315                 320

gtt gag aaa gaa cca cca aag atc tca aat aaa att gtt gtg tgg tcg   1008
Val Glu Lys Glu Pro Pro Lys Ile Ser Asn Lys Ile Val Val Trp Ser
                325                 330                 335

gtg ggt gtg atc ttc tat cag tgt ctt tct gga ggg aag cct ttt ggc   1056
Val Gly Val Ile Phe Tyr Gln Cys Leu Ser Gly Gly Lys Pro Phe Gly
            340                 345                 350

tat aac cag tct cag caa gac atc cta caa gag aat act att ctt aaa   1104
Tyr Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys
        355                 360                 365

gct gct gaa gag gag tca gtc ttg ctt tct cag ggg tgg cag agg cag   1152
Ala Ala Glu Glu Glu Ser Val Leu Leu Ser Gln Gly Trp Gln Arg Gln
    370                 375                 380

aag tgg agg aga tgg aag gga ggc agg aga ggc aaa cac acg tgg tat   1200
Lys Trp Arg Arg Trp Lys Gly Gly Arg Arg Gly Lys His Thr Trp Tyr
385                 390                 395                 400

aac ttt cca gaa cta cat cat aat ttc tgt ctg atg ctt ttt gct ttt   1248
Asn Phe Pro Glu Leu His His Asn Phe Cys Leu Met Leu Phe Ala Phe
                405                 410                 415

cta aaa agg tat ctg tac agt aac agt cct att gtt tgt ttt gat ttc   1296
Leu Lys Arg Tyr Leu Tyr Ser Asn Ser Pro Ile Val Cys Phe Asp Phe
            420                 425                 430

agc acc tgt att ata aaa ggt ttt aat ttt gtt gat gtt caa ttt att   1344
Ser Thr Cys Ile Ile Lys Gly Phe Asn Phe Val Asp Val Gln Phe Ile
        435                 440                 445

cat ttt ttc ttt ggg tcc ctg act tcc tgc aac aac ata tct ttt ctg   1392
His Phe Phe Phe Gly Ser Leu Thr Ser Cys Asn Asn Ile Ser Phe Leu
    450                 455                 460

tct tct act ttt ttt cat tgg aac cca aca gaa tca aac tca aac att   1440
Ser Ser Thr Phe Phe His Trp Asn Pro Thr Glu Ser Asn Ser Asn Ile
465                 470                 475                 480

aaa atc ctt act tta                                             1455
Lys Ile Leu Thr Leu
                485
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<210> 62
<211> 485
<212> PRT
<213> Homo sapiens

<400> 62

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Met Asn Val Met His Val Gly Asn Pro Ser Ala Thr Asp Gln Pro Ser
 1               5                  10                  15
Leu Cys Ile Arg Glu His Thr Gln Gly Arg Asn His Arg Gln Arg Lys
            20                  25                  30
Met Leu Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Asp Pro Pro Ala
        35                  40                  45
```

```
Thr Ser Glu Gln Lys Gln Trp Lys Ser Arg Thr Asn Gly Ala Glu Asn
    50                  55                  60
Lys Thr Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys
65                  70                  75                  80
Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu
                85                  90                  95
Leu Glu Arg Leu Glu Arg Val Arg Asn Leu Arg Ile Gly Glu Leu Lys
            100                 105                 110
Arg Ile His Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro Met Leu
        115                 120                 125
Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Asp Arg Gly Gly Phe Ser
    130                 135                 140
Lys Val Tyr Lys Ala Phe Glu Leu Ile Glu Gln Arg Tyr Val Ala Val
145                 150                 155                 160
Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn
                165                 170                 175
Tyr His Lys His Ala Cys Arg Glu Tyr Trp Ile His Lys Glu Leu Asp
            180                 185                 190
His Pro Arg Ile Ile Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp
        195                 200                 205
Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asn Phe
    210                 215                 220
Tyr Leu Lys Arg His Lys Leu Met Ser Glu Lys Glu Ala Trp Ser Ile
225                 230                 235                 240
Ile Met Gln Thr Val Asn Ala Leu Lys Tyr Leu Asn Lys Ile Lys Pro
                245                 250                 255
Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn
            260                 265                 270
Gly Thr Val Cys Gly Glu Arg Lys Ile Thr Glu Leu Gly Leu Ser Lys
        275                 280                 285
Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Gly Gly Met Glu Leu Thr
    290                 295                 300
Ser Gln Gly Ala Gly Thr Tyr Cys Asn Leu Thr Pro Glu Ser Phe Val
305                 310                 315                 320
Val Glu Lys Glu Pro Pro Lys Ile Ser Asn Lys Ile Val Val Trp Ser
                325                 330                 335
Val Gly Val Ile Phe Tyr Gln Cys Leu Ser Gly Gly Lys Pro Phe Gly
            340                 345                 350
Tyr Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys
        355                 360                 365
Ala Ala Glu Glu Glu Ser Val Leu Leu Ser Gln Gly Trp Gln Arg Gln
    370                 375                 380
Lys Trp Arg Arg Trp Lys Gly Gly Arg Arg Gly Lys His Thr Trp Tyr
385                 390                 395                 400
Asn Phe Pro Glu Leu His His Asn Phe Cys Leu Met Leu Phe Ala Phe
                405                 410                 415
Leu Lys Arg Tyr Leu Tyr Ser Asn Ser Pro Ile Val Cys Phe Asp Phe
            420                 425                 430
Ser Thr Cys Ile Ile Lys Gly Phe Asn Phe Val Asp Val Gln Phe Ile
        435                 440                 445
His Phe Phe Phe Gly Ser Leu Thr Ser Cys Asn Asn Ile Ser Phe Leu
    450                 455                 460
Ser Ser Thr Phe Phe His Trp Asn Pro Thr Glu Ser Asn Ser Asn Ile
465                 470                 475                 480
Lys Ile Leu Thr Leu
                485
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<210> 63
<211> 1323
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<213> Homo sapiens

<220>
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<222> (1)...(1323)
<223> MOOSE08757

<400> 63

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Ser Ile Val Ile Asn His Ile Ser Val Ser Val Ser Glu Leu Thr Arg
 1               5                  10                  15

ata aat aag aac gca aaa ata aaa aca cac acc cac agc cat ctg atc   96
Ile Asn Lys Asn Ala Lys Ile Lys Thr His Thr His Ser His Leu Ile
            20                  25                  30

ttc aac caa gtc gac aaa agt aag caa tgg gga aag gac acc cta gta   144
Phe Asn Gln Val Asp Lys Ser Lys Gln Trp Gly Lys Asp Thr Leu Val
        35                  40                  45

aat aaa tgg atg aca aac aac agc ggc tcc aaa gcc gaa ctc gtt gtg   192
Asn Lys Trp Met Thr Asn Asn Ser Gly Ser Lys Ala Glu Leu Val Val
    50                  55                  60

gga ggg aaa tac aaa ctg gtg cgg aag atc ggg tct ggc tcc ttt gga   240
Gly Gly Lys Tyr Lys Leu Val Arg Lys Ile Gly Ser Gly Ser Phe Gly
65                  70                  75                  80

gac gtt tat ctg ggc atc acc acc acc aac ggc gag gac gta gca gtg   288
Asp Val Tyr Leu Gly Ile Thr Thr Thr Asn Gly Glu Asp Val Ala Val
                85                  90                  95

aag ctg gaa tct cag aag gtc aag cac ccc cag ttg ctg tat gag agc   336
Lys Leu Glu Ser Gln Lys Val Lys His Pro Gln Leu Leu Tyr Glu Ser
            100                 105                 110

aaa ctc tac acg att ctt caa ggt ggg gtt ggc atc ccc cac atg cac   384
Lys Leu Tyr Thr Ile Leu Gln Gly Gly Val Gly Ile Pro His Met His
        115                 120                 125

tgg tat ggt cag gaa aaa gac aac aat gtg cta gtc atg gac ctt ctg   432
Trp Tyr Gly Gln Glu Lys Asp Asn Asn Val Leu Val Met Asp Leu Leu
    130                 135                 140

gga ccc agc ctc gaa gac ctc ttt aat ttc tgt tca aga agg ttc acc   480
Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys Ser Arg Arg Phe Thr
145                 150                 155                 160

atg aaa act gta ctt atg tta gcc gac cag atg atc agc aga att gaa   528
Met Lys Thr Val Leu Met Leu Ala Asp Gln Met Ile Ser Arg Ile Glu
                165                 170                 175

tac gtg cat aca aag aat ttt cta cac cga gac att aaa cca gat aac   576
Tyr Val His Thr Lys Asn Phe Leu His Arg Asp Ile Lys Pro Asp Asn
            180                 185                 190

ttc ctg atg ggt act ggg cgt cac tgt aat aag ttg ttc ctt att gat   624
Phe Leu Met Gly Thr Gly Arg His Cys Asn Lys Leu Phe Leu Ile Asp
        195                 200                 205

ttt ggt ttg gcc aaa aag tac aga gac aac agg acc agg caa cac ata   672
Phe Gly Leu Ala Lys Lys Tyr Arg Asp Asn Arg Thr Arg Gln His Ile
    210                 215                 220
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ccg tac aga gaa gat aaa cac ctc att ggc act gtc cga tat gcc agc   720
Pro Tyr Arg Glu Asp Lys His Leu Ile Gly Thr Val Arg Tyr Ala Ser
225                 230                 235                 240

atc aat gca cat ctt ggt att gag cag agc cgc cga gat gac atg gaa   768
Ile Asn Ala His Leu Gly Ile Glu Gln Ser Arg Arg Asp Asp Met Glu
                245                 250                 255

tcc tta ggc tac gtt ttc atg tat ttt aat aga acc agc ctg ccg tgg   816
Ser Leu Gly Tyr Val Phe Met Tyr Phe Asn Arg Thr Ser Leu Pro Trp
            260                 265                 270

caa gga cta agg gct atg aca aaa aaa caa aaa tat gaa aag att agt   864
Gln Gly Leu Arg Ala Met Thr Lys Lys Gln Lys Tyr Glu Lys Ile Ser
        275                 280                 285

gag aag aag atg tcc acc cct gtt gaa gtt tta tgt aag ggg ttt cct   912
Glu Lys Lys Met Ser Thr Pro Val Glu Val Leu Cys Lys Gly Phe Pro
    290                 295                 300

gca gaa ttc gcc atg tac ttg aac tac tgt cgt ggg ctg cgc ttt gag   960
Ala Glu Phe Ala Met Tyr Leu Asn Tyr Cys Arg Gly Leu Arg Phe Glu
305                 310                 315                 320

gaa gtc cca gat tac atg tat ctg agg cag cta ttc cgc att ctt ttc   1008
Glu Val Pro Asp Tyr Met Tyr Leu Arg Gln Leu Phe Arg Ile Leu Phe
                325                 330                 335

agg acc ctg aac cac caa tat gac tac aca ttt gat tgg acg atg tta   1056
Arg Thr Leu Asn His Gln Tyr Asp Tyr Thr Phe Asp Trp Thr Met Leu
            340                 345                 350

aag cag aaa gca gca cag cag gca gcc tct tcc agt ggg cag ggt cag   1104
Lys Gln Lys Ala Ala Gln Gln Ala Ala Ser Ser Ser Gly Gln Gly Gln
        355                 360                 365

cag gcc caa acc cag aca ggc aag caa act gaa aaa aac aag aat aat   1152
Gln Ala Gln Thr Gln Thr Gly Lys Gln Thr Glu Lys Asn Lys Asn Asn
    370                 375                 380

ctt tgt aaa aca aaa tat agg tgt ttt tgt cct agt ata tca tta ttc   1200
Leu Cys Lys Thr Lys Tyr Arg Cys Phe Cys Pro Ser Ile Ser Leu Phe
385                 390                 395                 400

cat ttt tct tct aga tac cat tca ttg tct tca cag ttc aca aaa gaa   1248
His Phe Ser Ser Arg Tyr His Ser Leu Ser Ser Gln Phe Thr Lys Glu
                405                 410                 415

gaa tac aag cct ggg caa cat ggt gaa acc tca tct cta cta aaa aat   1296
Glu Tyr Lys Pro Gly Gln His Gly Glu Thr Ser Ser Leu Leu Lys Asn
            420                 425                 430

aca aaa agt agc cag gca tgg tgg tgg                              1323
Thr Lys Ser Ser Gln Ala Trp Trp Trp
        435                 440
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<211> 441
<212> PRT
<213> Homo sapiens

<400> 64
Ser Ile Val Ile Asn His Ile Ser Val Ser Val Ser Glu Leu Thr Arg
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Ile Asn Lys Asn Ala Lys Ile Lys Thr His Thr His Ser His Leu Ile
20 25 30
Phe Asn Gln Val Asp Lys Ser Lys Gln Trp Gly Lys Asp Thr Leu Val
35 40 45
Asn Lys Trp Met Thr Asn Asn Ser Gly Ser Lys Ala Glu Leu Val Val
50 55 60
Gly Gly Lys Tyr Lys Leu Val Arg Lys Ile Gly Ser Gly Ser Phe Gly
65 70 75 80
Asp Val Tyr Leu Gly Ile Thr Thr Thr Asn Gly Glu Asp Val Ala Val
85 90 95
Lys Leu Glu Ser Gln Lys Val Lys His Pro Gln Leu Leu Tyr Glu Ser
100 105 110
Lys Leu Tyr Thr Ile Leu Gln Gly Gly Val Gly Ile Pro His Met His
115 120 125
Trp Tyr Gly Gln Glu Lys Asp Asn Asn Val Leu Val Met Asp Leu Leu
130 135 140
Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys Ser Arg Arg Phe Thr
145 150 155 160
Met Lys Thr Val Leu Met Leu Ala Asp Gln Met Ile Ser Arg Ile Glu
165 170 175
Tyr Val His Thr Lys Asn Phe Leu His Arg Asp Ile Lys Pro Asp Asn
180 185 190
Phe Leu Met Gly Thr Gly Arg His Cys Asn Lys Leu Phe Leu Ile Asp
195 200 205
Phe Gly Leu Ala Lys Lys Tyr Arg Asp Asn Arg Thr Arg Gln His Ile
210 215 220
Pro Tyr Arg Glu Asp Lys His Leu Ile Gly Thr Val Arg Tyr Ala Ser
225 230 235 240
Ile Asn Ala His Leu Gly Ile Glu Gln Ser Arg Arg Asp Asp Met Glu
245 250 255
Ser Leu Gly Tyr Val Phe Met Tyr Phe Asn Arg Thr Ser Leu Pro Trp
260 265 270
Gln Gly Leu Arg Ala Met Thr Lys Lys Gln Lys Tyr Glu Lys Ile Ser
275 280 285
Glu Lys Lys Met Ser Thr Pro Val Glu Val Leu Cys Lys Gly Phe Pro
290 295 300
Ala Glu Phe Ala Met Tyr Leu Asn Tyr Cys Arg Gly Leu Arg Phe Glu
305 310 315 320
Glu Val Pro Asp Tyr Met Tyr Leu Arg Gln Leu Phe Arg Ile Leu Phe
325 330 335
Arg Thr Leu Asn His Gln Tyr Asp Tyr Thr Phe Asp Trp Thr Met Leu
340 345 350
Lys Gln Lys Ala Ala Gln Gln Ala Ala Ser Ser Ser Gly Gln Gly Gln
355 360 365
Gln Ala Gln Thr Gln Thr Gly Lys Gln Thr Glu Lys Asn Lys Asn Asn
370 375 380
Leu Cys Lys Thr Lys Tyr Arg Cys Phe Cys Pro Ser Ile Ser Leu Phe
385 390 395 400
His Phe Ser Ser Arg Tyr His Ser Leu Ser Ser Gln Phe Thr Lys Glu
405 410 415
Glu Tyr Lys Pro Gly Gln His Gly Glu Thr Ser Ser Leu Leu Lys Asn
420 425 430
Thr Lys Ser Ser Gln Ala Trp Trp Trp
435 440

<210> 65
<211> 1779
<212> DNA

<213> Homo sapiens

<220>
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<222> (1)...(1779)
<223> MOOSE03397

<400> 65

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gtg gca gtg agc cga gat cac gcc act gca ctc cag cct ggg aga cag   48
Val Ala Val Ser Arg Asp His Ala Thr Ala Leu Gln Pro Gly Arg Gln
 1               5                  10                  15

gcg aga ctc cgt ctc aaa aaa aaa aaa aaa aaa aaa aaa gga aag aaa   96
Ala Arg Leu Arg Leu Lys Lys Lys Lys Lys Lys Lys Lys Gly Lys Lys
            20                  25                  30

gaa aga aag aag tca gct cag gac atg tgt caa ttg tac ccc gca gcc   144
Glu Arg Lys Lys Ser Ala Gln Asp Met Cys Gln Leu Tyr Pro Ala Ala
        35                  40                  45

cct caa gga aac cat cat tct ggg ttg agt cgc ccc ctg gtc gcc gcc   192
Pro Gln Gly Asn His His Ser Gly Leu Ser Arg Pro Leu Val Ala Ala
    50                  55                  60

ttc ctg cga gac ccg ggc tcg ggc cgc gtg tac agg cgc ggg aag ctg   240
Phe Leu Arg Asp Pro Gly Ser Gly Arg Val Tyr Arg Arg Gly Lys Leu
65                  70                  75                  80

atc ggc aag ggc gcc ttc agc cgc tgc tac aag ctg aca gac atg tcc   288
Ile Gly Lys Gly Ala Phe Ser Arg Cys Tyr Lys Leu Thr Asp Met Ser
                85                  90                  95

acc agc gcc gtg ttc gcc ctc aag gtg gtg ccg tgc ggg tac atg tcg   336
Thr Ser Ala Val Phe Ala Leu Lys Val Val Pro Cys Gly Tyr Met Ser
            100                 105                 110

ggg ccg tgc ctg cag gtg gag cgt gag att gcc ctg cat agc cgc ctg   384
Gly Pro Cys Leu Gln Val Glu Arg Glu Ile Ala Leu His Ser Arg Leu
        115                 120                 125

cga ccc cgc aac atc gtg gct ttc cac gga cac ttt gct gac cgc gac   432
Arg Pro Arg Asn Ile Val Ala Phe His Gly His Phe Ala Asp Arg Asp
    130                 135                 140

cac gtg tac atg gtg ctg gag tac tgc agc cgc cag tct ttg gcc cac   480
His Val Tyr Met Val Leu Glu Tyr Cys Ser Arg Gln Ser Leu Ala His
145                 150                 155                 160

gtg ctg agg gcg cgg cag atc ctg acg gag cca gaa gtg cgc gac tac   528
Val Leu Arg Ala Arg Gln Ile Leu Thr Glu Pro Glu Val Arg Asp Tyr
                165                 170                 175

ctg cgg ggc ctg gtc agc ggc ctg cgc tac ctg cac cag cgg tgc atc   576
Leu Arg Gly Leu Val Ser Gly Leu Arg Tyr Leu His Gln Arg Cys Ile
            180                 185                 190

ctg cac cgc gac ctg aag ctc agt aac ttc ttc ctt aac aag aac atg   624
Leu His Arg Asp Leu Lys Leu Ser Asn Phe Phe Leu Asn Lys Asn Met
        195                 200                 205
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gag gtg aag att gga gac ctg gga ctg gcg gcc aag gtg ggg cca ggg   672
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Lys Val Gly Pro Gly
    210                 215                 220

ggc cgc tgc cac aga gta ctc tgt ggg acc cct aac ttc ctg gac cct   720
Gly Arg Cys His Arg Val Leu Cys Gly Thr Pro Asn Phe Leu Asp Pro
225                 230                 235                 240

gag gtt gtc tcc aga aac ggt cac tcc tgc cag tac acg gtg ctg act   768
Glu Val Val Ser Arg Asn Gly His Ser Cys Gln Tyr Thr Val Leu Thr
                245                 250                 255

ggc acc cca ccc ttc atg gcc tca ccc ctg tcg gag atg tac caa aac   816
Gly Thr Pro Pro Phe Met Ala Ser Pro Leu Ser Glu Met Tyr Gln Asn
            260                 265                 270

atc cgt gag ggc cac tac ccc gaa ccc gct cac ctg tct gcc aat gcg   864
Ile Arg Glu Gly His Tyr Pro Glu Pro Ala His Leu Ser Ala Asn Ala
        275                 280                 285

cgc cgc ctc atc gtg cac ctc cta gca ccc aac ccg gcc gag cgg ccc   912
Arg Arg Leu Ile Val His Leu Leu Ala Pro Asn Pro Ala Glu Arg Pro
    290                 295                 300

agc ctg gac cac ctg ctg cag gac gac ttc ttc aca cag ggt ttc act   960
Ser Leu Asp His Leu Leu Gln Asp Asp Phe Phe Thr Gln Gly Phe Thr
305                 310                 315                 320

cca gac cgg ctg ccg gcc cac tcc tgc cac agt ccc ccc atc ttc gcc  1008
Pro Asp Arg Leu Pro Ala His Ser Cys His Ser Pro Pro Ile Phe Ala
                325                 330                 335

ata ccc ccg cct ctg ggc agg atc ttc cgg aag cct ggg gac aga gca  1056
Ile Pro Pro Pro Leu Gly Arg Ile Phe Arg Lys Pro Gly Asp Arg Ala
            340                 345                 350

aga ctc tgt ctc aaa aaa aca aaa caa aac aaa aca aac aaa aac aca  1104
Arg Leu Cys Leu Lys Lys Thr Lys Gln Asn Lys Thr Asn Lys Asn Thr
        355                 360                 365

cac acc cag aaa tgt gta gta ttt tca gag cat tgc aag tat ttg aga  1152
His Thr Gln Lys Cys Val Val Phe Ser Glu His Cys Lys Tyr Leu Arg
    370                 375                 380

att gct cat tcc cag ggg tgc gcc agt atc cca cag tct ccc tct gca  1200
Ile Ala His Ser Gln Gly Cys Ala Ser Ile Pro Gln Ser Pro Ser Ala
385                 390                 395                 400

agc cag aaa tta cag cag ccc atc ctc tgg gcc ccc aaa tgg gtg gat  1248
Ser Gln Lys Leu Gln Gln Pro Ile Leu Trp Ala Pro Lys Trp Val Asp
                405                 410                 415

tat tcc agc aaa tac ggc ttt ggc tac cag ctc ttg gac ggg ggg ggc  1296
Tyr Ser Ser Lys Tyr Gly Phe Gly Tyr Gln Leu Leu Asp Gly Gly Gly
            420                 425                 430

gca cgg gac ggc acc cac atg gcc ctg cga ccc ccc gga ggc caa gtg  1344
Ala Arg Asp Gly Thr His Met Ala Leu Arg Pro Pro Gly Gly Gln Val
        435                 440                 445
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tgc tac atg ccc aac tgc ggg agg ctg gaa gcc ttc gcc ctg agg gat   1392
Cys Tyr Met Pro Asn Cys Gly Arg Leu Glu Ala Phe Ala Leu Arg Asp
    450                 455                 460

gtg ccc ggc ctg ctg ggc gcc aag ctg gcc gtg ctg cag ctc ttt gcc   1440
Val Pro Gly Leu Leu Gly Ala Lys Leu Ala Val Leu Gln Leu Phe Ala
465                 470                 475                 480

ggc tgc ctg cgg cgg cgg ctg cgg gag gag ggg acc ctc ccc aca cct   1488
Gly Cys Leu Arg Arg Arg Leu Arg Glu Glu Gly Thr Leu Pro Thr Pro
                485                 490                 495

gtg cca cct gct gga ccc ggc ctc tgc ctc ctg cgc ttc ctg gcc tct   1536
Val Pro Pro Ala Gly Pro Gly Leu Cys Leu Leu Arg Phe Leu Ala Ser
            500                 505                 510

gag cac gcc ctg ctg ctg ctg ttc agc aat ggg atg gtg cag gtg agc   1584
Glu His Ala Leu Leu Leu Leu Phe Ser Asn Gly Met Val Gln Val Ser
        515                 520                 525

ttc agt gga gtc ccg gcc caa ctg gtg ctg agt ggc gag ggt gag ggt   1632
Phe Ser Gly Val Pro Ala Gln Leu Val Leu Ser Gly Glu Gly Glu Gly
    530                 535                 540

ttg cag ctc acc ctc tgg gag cag ggg tcc cct ggc acc tcc tac tcc   1680
Leu Gln Leu Thr Leu Trp Glu Gln Gly Ser Pro Gly Thr Ser Tyr Ser
545                 550                 555                 560

ctg gac gtc ccg cgg agc cac ggc tgc gcc ccc acc acc gga cag cac   1728
Leu Asp Val Pro Arg Ser His Gly Cys Ala Pro Thr Thr Gly Gln His
                565                 570                 575

ctt cac cac gcc ctc cgc atg ctg cag atg aga ctg aag aaa cca aag   1776
Leu His His Ala Leu Arg Met Leu Gln Met Arg Leu Lys Lys Pro Lys
            580                 585                 590

acc                                                               1779
Thr
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<210> 66
<211> 593
<212> PRT
<213> Homo sapiens

<400> 66

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Val Ala Val Ser Arg Asp His Ala Thr Ala Leu Gln Pro Gly Arg Gln
 1               5                  10                  15
Ala Arg Leu Arg Leu Lys Lys Lys Lys Lys Lys Lys Lys Gly Lys Lys
            20                  25                  30
Glu Arg Lys Lys Ser Ala Gln Asp Met Cys Gln Leu Tyr Pro Ala Ala
        35                  40                  45
Pro Gln Gly Asn His His Ser Gly Leu Ser Arg Pro Leu Val Ala Ala
    50                  55                  60
Phe Leu Arg Asp Pro Gly Ser Gly Arg Val Tyr Arg Arg Gly Lys Leu
65                  70                  75                  80
Ile Gly Lys Gly Ala Phe Ser Arg Cys Tyr Lys Leu Thr Asp Met Ser
                85                  90                  95
Thr Ser Ala Val Phe Ala Leu Lys Val Val Pro Cys Gly Tyr Met Ser
            100                 105                 110
```

```
Gly Pro Cys Leu Gln Val Glu Arg Glu Ile Ala Leu His Ser Arg Leu
        115                 120                 125
Arg Pro Arg Asn Ile Val Ala Phe His Gly His Phe Ala Asp Arg Asp
    130                 135                 140
His Val Tyr Met Val Leu Glu Tyr Cys Ser Arg Gln Ser Leu Ala His
145                 150                 155                 160
Val Leu Arg Ala Arg Gln Ile Leu Thr Glu Pro Glu Val Arg Asp Tyr
                165                 170                 175
Leu Arg Gly Leu Val Ser Gly Leu Arg Tyr Leu His Gln Arg Cys Ile
            180                 185                 190
Leu His Arg Asp Leu Lys Leu Ser Asn Phe Phe Leu Asn Lys Asn Met
        195                 200                 205
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Lys Val Gly Pro Gly
    210                 215                 220
Gly Arg Cys His Arg Val Leu Cys Gly Thr Pro Asn Phe Leu Asp Pro
225                 230                 235                 240
Glu Val Val Ser Arg Asn Gly His Ser Cys Gln Tyr Thr Val Leu Thr
                245                 250                 255
Gly Thr Pro Pro Phe Met Ala Ser Pro Leu Ser Glu Met Tyr Gln Asn
            260                 265                 270
Ile Arg Glu Gly His Tyr Pro Glu Pro Ala His Leu Ser Ala Asn Ala
        275                 280                 285
Arg Arg Leu Ile Val His Leu Leu Ala Pro Asn Pro Ala Glu Arg Pro
    290                 295                 300
Ser Leu Asp His Leu Leu Gln Asp Asp Phe Phe Thr Gln Gly Phe Thr
305                 310                 315                 320
Pro Asp Arg Leu Pro Ala His Ser Cys His Ser Pro Pro Ile Phe Ala
                325                 330                 335
Ile Pro Pro Pro Leu Gly Arg Ile Phe Arg Lys Pro Gly Asp Arg Ala
            340                 345                 350
Arg Leu Cys Leu Lys Lys Thr Lys Gln Asn Lys Thr Asn Lys Asn Thr
        355                 360                 365
His Thr Gln Lys Cys Val Val Phe Ser Glu His Cys Lys Tyr Leu Arg
    370                 375                 380
Ile Ala His Ser Gln Gly Cys Ala Ser Ile Pro Gln Ser Pro Ser Ala
385                 390                 395                 400
Ser Gln Lys Leu Gln Gln Pro Ile Leu Trp Ala Pro Lys Trp Val Asp
                405                 410                 415
Tyr Ser Ser Lys Tyr Gly Phe Gly Tyr Gln Leu Leu Asp Gly Gly Gly
            420                 425                 430
Ala Arg Asp Gly Thr His Met Ala Leu Arg Pro Pro Gly Gly Gln Val
        435                 440                 445
Cys Tyr Met Pro Asn Cys Gly Arg Leu Glu Ala Phe Ala Leu Arg Asp
    450                 455                 460
Val Pro Gly Leu Leu Gly Ala Lys Leu Ala Val Leu Gln Leu Phe Ala
465                 470                 475                 480
Gly Cys Leu Arg Arg Arg Leu Arg Glu Glu Gly Thr Leu Pro Thr Pro
                485                 490                 495
Val Pro Pro Ala Gly Pro Gly Leu Cys Leu Leu Arg Phe Leu Ala Ser
            500                 505                 510
Glu His Ala Leu Leu Leu Leu Phe Ser Asn Gly Met Val Gln Val Ser
        515                 520                 525
Phe Ser Gly Val Pro Ala Gln Leu Val Leu Ser Gly Glu Gly Glu Gly
    530                 535                 540
Leu Gln Leu Thr Leu Trp Glu Gln Gly Ser Pro Gly Thr Ser Tyr Ser
545                 550                 555                 560
Leu Asp Val Pro Arg Ser His Gly Cys Ala Pro Thr Thr Gly Gln His
                565                 570                 575
Leu His His Ala Leu Arg Met Leu Gln Met Arg Leu Lys Lys Pro Lys
            580                 585                 590
Thr
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<210> 67
<211> 2307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2307)
<223> MOOSE03609

<400> 67

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Leu Ala Gly Tyr Glu Ile Leu Gly Cys Lys Phe Phe Ser Phe Arg Met
 1               5                  10                  15

ttg aat att ggc ccc cac tct ctt ctg gct tgt aga gtt tct gcg gag   96
Leu Asn Ile Gly Pro His Ser Leu Leu Ala Cys Arg Val Ser Ala Glu
            20                  25                  30

aga tca gct gtt agt ctg atg gca atg agc aag gct ccg tgg gca tgg   144
Arg Ser Ala Val Ser Leu Met Ala Met Ser Lys Ala Pro Trp Ala Trp
        35                  40                  45

cac cct cta agc cag tgg gat gcc atc act gaa atg gat gaa cat aat   192
His Pro Leu Ser Gln Trp Asp Ala Ile Thr Glu Met Asp Glu His Asn
    50                  55                  60

agg ccc att cac aca tac cag gta tgt aat gta atg gaa cca aac caa   240
Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu Pro Asn Gln
65                  70                  75                  80

aac aac tgg ctt cgt aca aac tgg atc tcc cgt gat gca gct cag aaa   288
Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys
                85                  90                  95

att tat gtg gaa atg aaa ttc aca cta agg gat tgt aac agc atc cca   336
Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro
            100                 105                 110

tgg gtc ttg ggg act tgc aaa gaa aca ttt aat ctg ttt tat atg gaa   384
Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu
        115                 120                 125

tca gat gag tcc cac gga att aaa ttc aag cca aac cag tat aca aag   432
Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys
    130                 135                 140

atc gac aca att gct gct gat gag agt ttt acc cag atg gat ttg ggt   480
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly
145                 150                 155                 160

gat cgc atc ctc aaa ctc aac act gaa att cgt gag gtg ggg cct ata   528
Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Ile
                165                 170                 175

gaa agg aaa gga ttt tat ctg gct ttt caa gac att ggg gcg tgc att   576
Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile
            180                 185                 190
```

```
gcc ctg gtt tca gtc cgt gtt ttc tac aag aaa tgc ccc ttc act gtt   624
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Phe Thr Val
        195                 200                 205

cgt aac ttg gcc atg ttt cct gat acc att cca agg gtt gat tcc tcc   672
Arg Asn Leu Ala Met Phe Pro Asp Thr Ile Pro Arg Val Asp Ser Ser
    210                 215                 220

tct ttg gtt gaa gta cgg ggt tct tgt gtg aag agt gct gaa gag cgt   720
Ser Leu Val Glu Val Arg Gly Ser Cys Val Lys Ser Ala Glu Glu Arg
225                 230                 235                 240

gac act cct aaa ctg tat tgt gga gct gat gga gat tgg ctg gtt cct   768
Asp Thr Pro Lys Leu Tyr Cys Gly Ala Asp Gly Asp Trp Leu Val Pro
                245                 250                 255

ctt gga agg tgc atc tgc agt aca gga tat gaa gaa att gag ggt tct   816
Leu Gly Arg Cys Ile Cys Ser Thr Gly Tyr Glu Glu Ile Glu Gly Ser
            260                 265                 270

tgc cat gac tgt cat att gga cat ttt gtg ttt aaa att tta gac ctg   864
Cys His Asp Cys His Ile Gly His Phe Val Phe Lys Ile Leu Asp Leu
        275                 280                 285

ctg aga atg tgt gtg tgt atg tgt gta aat ggg ata tac agg gcc ttt   912
Leu Arg Met Cys Val Cys Met Cys Val Asn Gly Ile Tyr Arg Ala Phe
    290                 295                 300

aga gat cct ttc ccc att gct tgt ttt tgt cag gtt tgt caa gga tca   960
Arg Asp Pro Phe Pro Ile Ala Cys Phe Cys Gln Val Cys Gln Gly Ser
305                 310                 315                 320

gat ggt tgt aga tgt gtg gtc agt atg gcc att ttc aca tta ttg aat   1008
Asp Gly Cys Arg Cys Val Val Ser Met Ala Ile Phe Thr Leu Leu Asn
                325                 330                 335

ctt cgt atc cat gag gat gga atg ttt tcc cat ttc tct tat tat ttt   1056
Leu Arg Ile His Glu Asp Gly Met Phe Ser His Phe Ser Tyr Tyr Phe
            340                 345                 350

gag atg cat tct ggc tgc ata ctg cca cag cca gta ttt tgg gct gtg   1104
Glu Met His Ser Gly Cys Ile Leu Pro Gln Pro Val Phe Trp Ala Val
        355                 360                 365

ggg aca agt ctt ggg acc aaa cca tcc agc ctc cct ggc tct ggc agg   1152
Gly Thr Ser Leu Gly Thr Lys Pro Ser Ser Leu Pro Gly Ser Gly Arg
    370                 375                 380

gga aaa gag cag cct aga gct ata gaa atg ggt gct gcc ctt ccc cca   1200
Gly Lys Glu Gln Pro Arg Ala Ile Glu Met Gly Ala Ala Leu Pro Pro
385                 390                 395                 400

tcc agg gag ctt agt gtg gta ggc agt tgc cag att tca tat tta ttt   1248
Ser Arg Glu Leu Ser Val Val Gly Ser Cys Gln Ile Ser Tyr Leu Phe
                405                 410                 415

gtc ttc gga aag aat ttg gtt ttt att aaa atg cag aaa tat ctg aga   1296
Val Phe Gly Lys Asn Leu Val Phe Ile Lys Met Gln Lys Tyr Leu Arg
            420                 425                 430
```

```
gag att gtt agt aaa aaa tgt agg gat gtg tat gtg gtg cgt gtg tgt   1344
Glu Ile Val Ser Lys Lys Cys Arg Asp Val Tyr Val Val Arg Val Cys
        435                 440                 445

gtg ttc aaa gat cac ggt tat ggc aag gtt agt ttc tgg tgg gga tgc   1392
Val Phe Lys Asp His Gly Tyr Gly Lys Val Ser Phe Trp Trp Gly Cys
    450                 455                 460

tct tcc tta ctt gca gaa gcc cac att ctt gct gtg tca tca cat ggt   1440
Ser Ser Leu Leu Ala Glu Ala His Ile Leu Ala Val Ser Ser His Gly
465                 470                 475                 480

ttt tcc tct gtg ctt gtg cac ttg tct ctt ctt ctt atc agg aca aca   1488
Phe Ser Ser Val Leu Val His Leu Ser Leu Leu Leu Ile Arg Thr Thr
                485                 490                 495

atc cta ttg tgt att gta act cta cag gac atg tct gac cct gtt cac   1536
Ile Leu Leu Cys Ile Val Thr Leu Gln Asp Met Ser Asp Pro Val His
            500                 505                 510

tca tca cta aaa tta cta tat aca acc aga att gtg ctt gac aca tat   1584
Ser Ser Leu Lys Leu Leu Tyr Thr Thr Arg Ile Val Leu Asp Thr Tyr
        515                 520                 525

aat gaa gca ttg aga aaa cat ttg agc tca ata aaa gtg tct tcc ttt   1632
Asn Glu Ala Leu Arg Lys His Leu Ser Ser Ile Lys Val Ser Ser Phe
    530                 535                 540

ctt ttg tct tct tta ata ggt ggt atg atc act atg gat atc aaa atg   1680
Leu Leu Ser Ser Leu Ile Gly Gly Met Ile Thr Met Asp Ile Lys Met
545                 550                 555                 560

gga agt tac agt cat cct tat tat ata aga ata cag gga atc ctg agc   1728
Gly Ser Tyr Ser His Pro Tyr Tyr Ile Arg Ile Gln Gly Ile Leu Ser
                565                 570                 575

aag cgg tat tat gag gag gct gct gga gac tcg gta ctc ttg gaa agg   1776
Lys Arg Tyr Tyr Glu Glu Ala Ala Gly Asp Ser Val Leu Leu Glu Arg
            580                 585                 590

ttc ata agc agt cta ctg aaa tgg tta tgt gca cac aca cac ata cac   1824
Phe Ile Ser Ser Leu Leu Lys Trp Leu Cys Ala His Thr His Ile His
        595                 600                 605

ata cag agt act gtt tct atg ttc cag att gaa ttt ttt cct gaa aag   1872
Ile Gln Ser Thr Val Ser Met Phe Gln Ile Glu Phe Phe Pro Glu Lys
    610                 615                 620

aag tac aca agc act cca gca att tcc act ata aaa ttt ccc ttt tgg   1920
Lys Tyr Thr Ser Thr Pro Ala Ile Ser Thr Ile Lys Phe Pro Phe Trp
625                 630                 635                 640

ggc atg aaa aat aat gtt tgc aga agc att gaa tgt tgg gta aga gga   1968
Gly Met Lys Asn Asn Val Cys Arg Ser Ile Glu Cys Trp Val Arg Gly
                645                 650                 655

gaa agt ggc agg aaa aca aga agg cct aag act caa cat ata aag gaa   2016
Glu Ser Gly Arg Lys Thr Arg Arg Pro Lys Thr Gln His Ile Lys Glu
            660                 665                 670
```

```
gtt aat aaa gga gag aaa atg ata gcc cct cct cca aca cta caa att   2064
Val Asn Lys Gly Glu Lys Met Ile Ala Pro Pro Pro Thr Leu Gln Ile
        675                 680                 685

aca att caa cat aag att tgg gta ggg aca caa atc caa acc atg tca   2112
Thr Ile Gln His Lys Ile Trp Val Gly Thr Gln Ile Gln Thr Met Ser
    690                 695                 700

gta cct gat acc tca atc tat aga gat gtt tcc cag tct ttt gaa tat   2160
Val Pro Asp Thr Ser Ile Tyr Arg Asp Val Ser Gln Ser Phe Glu Tyr
705                 710                 715                 720

att gtc ata caa aga aat ata tct gaa ttt gtc cac act ggt tgg aaa   2208
Ile Val Ile Gln Arg Asn Ile Ser Glu Phe Val His Thr Gly Trp Lys
                725                 730                 735

tcc caa ata tat gca gaa cta aaa tgt tta gca ggg cac tca tgt aga   2256
Ser Gln Ile Tyr Ala Glu Leu Lys Cys Leu Ala Gly His Ser Cys Arg
            740                 745                 750

gtt tta tcc ttc ata cat gta cag atg atg ctt tcc aaa cct aga ata   2304
Val Leu Ser Phe Ile His Val Gln Met Met Leu Ser Lys Pro Arg Ile
        755                 760                 765

cct                                                               2307
Pro
```

<210> 68
<211> 769
<212> PRT
<213> Homo sapiens

<400> 68

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Leu Ala Gly Tyr Glu Ile Leu Gly Cys Lys Phe Phe Ser Phe Arg Met
 1               5                  10                  15
Leu Asn Ile Gly Pro His Ser Leu Leu Ala Cys Arg Val Ser Ala Glu
            20                  25                  30
Arg Ser Ala Val Ser Leu Met Ala Met Ser Lys Ala Pro Trp Ala Trp
        35                  40                  45
His Pro Leu Ser Gln Trp Asp Ala Ile Thr Glu Met Asp Glu His Asn
    50                  55                  60
Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu Pro Asn Gln
65                  70                  75                  80
Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys
                85                  90                  95
Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro
            100                 105                 110
Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu
        115                 120                 125
Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys
    130                 135                 140
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly
145                 150                 155                 160
Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Ile
                165                 170                 175
Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile
            180                 185                 190
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Phe Thr Val
        195                 200                 205
```

```
Arg Asn Leu Ala Met Phe Pro Asp Thr Ile Pro Arg Val Asp Ser Ser
    210                 215                 220
Ser Leu Val Glu Val Arg Gly Ser Cys Val Lys Ser Ala Glu Glu Arg
225                 230                 235                 240
Asp Thr Pro Lys Leu Tyr Cys Gly Ala Asp Gly Asp Trp Leu Val Pro
                245                 250                 255
Leu Gly Arg Cys Ile Cys Ser Thr Gly Tyr Glu Glu Ile Glu Gly Ser
            260                 265                 270
Cys His Asp Cys His Ile Gly His Phe Val Phe Lys Ile Leu Asp Leu
        275                 280                 285
Leu Arg Met Cys Val Cys Met Cys Val Asn Gly Ile Tyr Arg Ala Phe
    290                 295                 300
Arg Asp Pro Phe Pro Ile Ala Cys Phe Cys Gln Val Cys Gln Gly Ser
305                 310                 315                 320
Asp Gly Cys Arg Cys Val Val Ser Met Ala Ile Phe Thr Leu Leu Asn
                325                 330                 335
Leu Arg Ile His Glu Asp Gly Met Phe Ser His Phe Ser Tyr Tyr Phe
            340                 345                 350
Glu Met His Ser Gly Cys Ile Leu Pro Gln Pro Val Phe Trp Ala Val
        355                 360                 365
Gly Thr Ser Leu Gly Thr Lys Pro Ser Ser Leu Pro Gly Ser Gly Arg
    370                 375                 380
Gly Lys Glu Gln Pro Arg Ala Ile Glu Met Gly Ala Ala Leu Pro Pro
385                 390                 395                 400
Ser Arg Glu Leu Ser Val Val Gly Ser Cys Gln Ile Ser Tyr Leu Phe
                405                 410                 415
Val Phe Gly Lys Asn Leu Val Phe Ile Lys Met Gln Lys Tyr Leu Arg
            420                 425                 430
Glu Ile Val Ser Lys Lys Cys Arg Asp Val Tyr Val Val Arg Val Cys
        435                 440                 445
Val Phe Lys Asp His Gly Tyr Gly Lys Val Ser Phe Trp Trp Gly Cys
    450                 455                 460
Ser Ser Leu Leu Ala Glu Ala His Ile Leu Ala Val Ser Ser His Gly
465                 470                 475                 480
Phe Ser Ser Val Leu Val His Leu Ser Leu Leu Leu Ile Arg Thr Thr
                485                 490                 495
Ile Leu Leu Cys Ile Val Thr Leu Gln Asp Met Ser Asp Pro Val His
            500                 505                 510
Ser Ser Leu Lys Leu Leu Tyr Thr Thr Arg Ile Val Leu Asp Thr Tyr
        515                 520                 525
Asn Glu Ala Leu Arg Lys His Leu Ser Ser Ile Lys Val Ser Ser Phe
    530                 535                 540
Leu Leu Ser Ser Leu Ile Gly Gly Met Ile Thr Met Asp Ile Lys Met
545                 550                 555                 560
Gly Ser Tyr Ser His Pro Tyr Tyr Ile Arg Ile Gln Gly Ile Leu Ser
                565                 570                 575
Lys Arg Tyr Tyr Glu Glu Ala Ala Gly Asp Ser Val Leu Leu Glu Arg
            580                 585                 590
Phe Ile Ser Ser Leu Leu Lys Trp Leu Cys Ala His Thr His Ile His
        595                 600                 605
Ile Gln Ser Thr Val Ser Met Phe Gln Ile Glu Phe Phe Pro Glu Lys
    610                 615                 620
Lys Tyr Thr Ser Thr Pro Ala Ile Ser Thr Ile Lys Phe Pro Phe Trp
625                 630                 635                 640
Gly Met Lys Asn Asn Val Cys Arg Ser Ile Glu Cys Trp Val Arg Gly
                645                 650                 655
Glu Ser Gly Arg Lys Thr Arg Arg Pro Lys Thr Gln His Ile Lys Glu
            660                 665                 670
Val Asn Lys Gly Glu Lys Met Ile Ala Pro Pro Pro Thr Leu Gln Ile
        675                 680                 685
Thr Ile Gln His Lys Ile Trp Val Gly Thr Gln Ile Gln Thr Met Ser
    690                 695                 700
```

```
Val Pro Asp Thr Ser Ile Tyr Arg Asp Val Ser Gln Ser Phe Glu Tyr
705                 710                 715                 720
Ile Val Ile Gln Arg Asn Ile Ser Glu Phe Val His Thr Gly Trp Lys
                725                 730                 735
Ser Gln Ile Tyr Ala Glu Leu Lys Cys Leu Ala Gly His Ser Cys Arg
            740                 745                 750
Val Leu Ser Phe Ile His Val Gln Met Met Leu Ser Lys Pro Arg Ile
        755                 760                 765
Pro
```

<210> 69
<211> 888
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(888)
<223> MOOSE03184

<400> 69

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gcc tca tct tac ttg aac ttg gag aag ctg ggt gaa ggc tct tat gcg   48
Ala Ser Ser Tyr Leu Asn Leu Glu Lys Leu Gly Glu Gly Ser Tyr Ala
 1               5                  10                  15

aca gtt tac aag ggg att agc aga ata aat gga caa cta gtg gct tta   96
Thr Val Tyr Lys Gly Ile Ser Arg Ile Asn Gly Gln Leu Val Ala Leu
            20                  25                  30

aaa gtc atc agc atg aat gca gag gaa gga gtc cca ttt aca gct atc   144
Lys Val Ile Ser Met Asn Ala Glu Glu Gly Val Pro Phe Thr Ala Ile
        35                  40                  45

cga gaa gct tct ctc ctg aag ggt ttg aaa cat gcc aat att gtg ctc   192
Arg Glu Ala Ser Leu Leu Lys Gly Leu Lys His Ala Asn Ile Val Leu
    50                  55                  60

ctg cat gac ata atc cac acc aaa gag aca ctg aca ttc gtt ttt gaa   240
Leu His Asp Ile Ile His Thr Lys Glu Thr Leu Thr Phe Val Phe Glu
65                  70                  75                  80

tac atg gtg agt tac ctg gcc cag tat atg tct cag cat cca gga ggg   288
Tyr Met Val Ser Tyr Leu Ala Gln Tyr Met Ser Gln His Pro Gly Gly
                85                  90                  95

ctt cat cct cat aat gtc aga ctt ttc atg ttt caa ctt ttg cgg ggc   336
Leu His Pro His Asn Val Arg Leu Phe Met Phe Gln Leu Leu Arg Gly
            100                 105                 110

ctg gcg tac atc cac cac caa cac gtt ctt cac agg gac ctg aaa cct   384
Leu Ala Tyr Ile His His Gln His Val Leu His Arg Asp Leu Lys Pro
        115                 120                 125

cag aac tta ctc atc agt cac ctg gga gag ctc aaa ctg gct gat ttt   432
Gln Asn Leu Leu Ile Ser His Leu Gly Glu Leu Lys Leu Ala Asp Phe
    130                 135                 140

ggt ctt gcc cgg gcc aag tcc att ccc agc cag aca tac tct tca gaa   480
Gly Leu Ala Arg Ala Lys Ser Ile Pro Ser Gln Thr Tyr Ser Ser Glu
145                 150                 155                 160
```

```
gtc gtg acc ctc tgg tac cgg ccc cct gat gct ttg ctg gga gcc act   528
Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ala Leu Leu Gly Ala Thr
                165                 170                 175

gaa tat tcc tct gag ctg gac ata tgg ggt gca ggc tgc atc ttt att   576
Glu Tyr Ser Ser Glu Leu Asp Ile Trp Gly Ala Gly Cys Ile Phe Ile
            180                 185                 190

gaa atg ttc cag ggt caa cct ttg ttt cct ggg gtt tcc aac atc ctt   624
Glu Met Phe Gln Gly Gln Pro Leu Phe Pro Gly Val Ser Asn Ile Leu
        195                 200                 205

gaa cag ctg gag aaa atc tgg gag gtg ctg gga gtc cct aca gag gat   672
Glu Gln Leu Glu Lys Ile Trp Glu Val Leu Gly Val Pro Thr Glu Asp
    210                 215                 220

act tgg ccg gga gtc tcc aag cta cct aac tac aat cca ggc tgc tgg   720
Thr Trp Pro Gly Val Ser Lys Leu Pro Asn Tyr Asn Pro Gly Cys Trp
225                 230                 235                 240

aga aac tct att ttt ctc tcc cac ttt tcc agg ctg ggc agg gtt cct   768
Arg Asn Ser Ile Phe Leu Ser His Phe Ser Arg Leu Gly Arg Val Pro
                245                 250                 255

gaa gct gaa gac ctg gcc tcc cag atg cta aaa ggc ttt ccc aga gac   816
Glu Ala Glu Asp Leu Ala Ser Gln Met Leu Lys Gly Phe Pro Arg Asp
            260                 265                 270

cgc gtc tcc gcc cag gaa gca ctt gtt cat gat tat ttc agc gcc ctg   864
Arg Val Ser Ala Gln Glu Ala Leu Val His Asp Tyr Phe Ser Ala Leu
        275                 280                 285

cca tct cag ctg tac cag ctt cct                                  888
Pro Ser Gln Leu Tyr Gln Leu Pro
    290                 295
```

<210> 70
<211> 296
<212> PRT
<213> Homo sapiens

<400> 70

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Ala Ser Ser Tyr Leu Asn Leu Glu Lys Leu Gly Glu Gly Ser Tyr Ala
 1               5                  10                  15
Thr Val Tyr Lys Gly Ile Ser Arg Ile Asn Gly Gln Leu Val Ala Leu
            20                  25                  30
Lys Val Ile Ser Met Asn Ala Glu Glu Gly Val Pro Phe Thr Ala Ile
        35                  40                  45
Arg Glu Ala Ser Leu Leu Lys Gly Leu Lys His Ala Asn Ile Val Leu
    50                  55                  60
Leu His Asp Ile Ile His Thr Lys Glu Thr Leu Thr Phe Val Phe Glu
65                  70                  75                  80
Tyr Met Val Ser Tyr Leu Ala Gln Tyr Met Ser Gln His Pro Gly Gly
                85                  90                  95
Leu His Pro His Asn Val Arg Leu Phe Met Phe Gln Leu Leu Arg Gly
            100                 105                 110
Leu Ala Tyr Ile His His Gln His Val Leu His Arg Asp Leu Lys Pro
        115                 120                 125
Gln Asn Leu Leu Ile Ser His Leu Gly Glu Leu Lys Leu Ala Asp Phe
    130                 135                 140
```

```
Gly Leu Ala Arg Ala Lys Ser Ile Pro Ser Gln Thr Tyr Ser Ser Glu
145                 150                 155                 160
Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ala Leu Leu Gly Ala Thr
                165                 170                 175
Glu Tyr Ser Ser Glu Leu Asp Ile Trp Gly Ala Gly Cys Ile Phe Ile
            180                 185                 190
Glu Met Phe Gln Gly Gln Pro Leu Phe Pro Gly Val Ser Asn Ile Leu
        195                 200                 205
Glu Gln Leu Glu Lys Ile Trp Glu Val Leu Gly Val Pro Thr Glu Asp
    210                 215                 220
Thr Trp Pro Gly Val Ser Lys Leu Pro Asn Tyr Asn Pro Gly Cys Trp
225                 230                 235                 240
Arg Asn Ser Ile Phe Leu Ser His Phe Ser Arg Leu Gly Arg Val Pro
                245                 250                 255
Glu Ala Glu Asp Leu Ala Ser Gln Met Leu Lys Gly Phe Pro Arg Asp
            260                 265                 270
Arg Val Ser Ala Gln Glu Ala Leu Val His Asp Tyr Phe Ser Ala Leu
        275                 280                 285
Pro Ser Gln Leu Tyr Gln Leu Pro
    290                 295


<210> 71
<211> 1098
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1098)
<223> MOOSE03305

<400> 71
att gcc gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg   48
Ile Ala Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly
 1               5                  10                  15

gat ggg aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg   96
Asp Gly Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg
            20                  25                  30

cag gcc tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag   144
Gln Ala Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys
        35                  40                  45

gag gac atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac   192
Glu Asp Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His
    50                  55                  60

ccc aac atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc   240
Pro Asn Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile
65                  70                  75                  80

tac ctg atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc   288
Tyr Leu Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile
                85                  90                  95

ata gaa agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg   336
Ile Glu Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met
            100                 105                 110
```

```
gac tta tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac   384
Asp Leu Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His
        115                 120                 125

cgg gac ctc aag ccg gaa aac ctt ttg cga aat gag gac aaa tct act   432
Arg Asp Leu Lys Pro Glu Asn Leu Leu Arg Asn Glu Asp Lys Ser Thr
    130                 135                 140

acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct   480
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
145                 150                 155                 160

ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt   528
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
                165                 170                 175

tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg   576
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
            180                 185                 190

atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag   624
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
        195                 200                 205

agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag   672
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
    210                 215                 220

ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg   720
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
225                 230                 235                 240

gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat   768
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
                245                 250                 255

cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca   816
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
            260                 265                 270

gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg   864
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
        275                 280                 285

agc cag cac aag agg gtt gtg gag cag gta tca tat gaa tct ata gtg   912
Ser Gln His Lys Arg Val Val Glu Gln Val Ser Tyr Glu Ser Ile Val
    290                 295                 300

aca gaa agt gat cag ggg gtt tgc tgg aga tgg aaa tgg gga gag gag   960
Thr Glu Ser Asp Gln Gly Val Cys Trp Arg Trp Lys Trp Gly Glu Glu
305                 310                 315                 320

gga cag aag gat tgc aag gga aca ctt ggt aac ttt ggg gaa gag gga  1008
Gly Gln Lys Asp Cys Lys Gly Thr Leu Gly Asn Phe Gly Glu Glu Gly
                325                 330                 335

cgt gtt cat ttt ctt gaa ttg tgg aga aga aat ggg gaa atg agt cca  1056
Arg Val His Phe Leu Glu Leu Trp Arg Arg Asn Gly Glu Met Ser Pro
            340                 345                 350
```

gga aga gag gaa ggc caa gaa aga gtg cat tca cgt gtg agg 1098
Gly Arg Glu Glu Gly Gln Glu Arg Val His Ser Arg Val Arg
355 360 365

<210> 72
<211> 366
<212> PRT
<213> Homo sapiens

<400> 72
Ile Ala Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly
1 5 10 15
Asp Gly Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg
20 25 30
Gln Ala Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys
35 40 45
Glu Asp Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His
50 55 60
Pro Asn Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile
65 70 75 80
Tyr Leu Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile
85 90 95
Ile Glu Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met
100 105 110
Asp Leu Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His
115 120 125
Arg Asp Leu Lys Pro Glu Asn Leu Leu Arg Asn Glu Asp Lys Ser Thr
130 135 140
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
145 150 155 160
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
165 170 175
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
180 185 190
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
195 200 205
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
210 215 220
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
225 230 235 240
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
245 250 255
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
260 265 270
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
275 280 285
Ser Gln His Lys Arg Val Val Glu Gln Val Ser Tyr Glu Ser Ile Val
290 295 300
Thr Glu Ser Asp Gln Gly Val Cys Trp Arg Trp Lys Trp Gly Glu Glu
305 310 315 320
Gly Gln Lys Asp Cys Lys Gly Thr Leu Gly Asn Phe Gly Glu Glu Gly
325 330 335
Arg Val His Phe Leu Glu Leu Trp Arg Arg Asn Gly Glu Met Ser Pro
340 345 350
Gly Arg Glu Glu Gly Gln Glu Arg Val His Ser Arg Val Arg
355 360 365

<210> 73
<211> 1407

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1407)
<223> MOOSE03302

<400> 73

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aaa ggt gtt gga aga ttt aaa gat cgg aaa tat gaa ata atc cga ttt   48
Lys Gly Val Gly Arg Phe Lys Asp Arg Lys Tyr Glu Ile Ile Arg Phe
 1               5                  10                  15

cat tat aca aag ctc tct ctt gct gca gtg tgg caa ggg att ata gga   96
His Tyr Thr Lys Leu Ser Leu Ala Ala Val Trp Gln Gly Ile Ile Gly
            20                  25                  30

ggg cag aat gga agt gga gga aaa tgg ata ttg gag gag tca aag aaa   144
Gly Gln Asn Gly Ser Gly Gly Lys Trp Ile Leu Glu Glu Ser Lys Lys
        35                  40                  45

aaa aat gac aat gat ttg ggc ata ggt gag agc agt aga gga gaa aac   192
Lys Asn Asp Asn Asp Leu Gly Ile Gly Glu Ser Ser Arg Gly Glu Asn
    50                  55                  60

tta tgt ttc atc ttc aaa agc tca gta aga gtg tgc cac gtt atg gag   240
Leu Cys Phe Ile Phe Lys Ser Ser Val Arg Val Cys His Val Met Glu
65                  70                  75                  80

gtc cat gca tat acg ggg tct cac tat gtt gcc cag act gaa ttc ctg   288
Val His Ala Tyr Thr Gly Ser His Tyr Val Ala Gln Thr Glu Phe Leu
                85                  90                  95

ggc tca agt gat cct cct gcc ttg gcc tcc caa aat gct gag gtt aca   336
Gly Ser Ser Asp Pro Pro Ala Leu Ala Ser Gln Asn Ala Glu Val Thr
            100                 105                 110

agc ctg agc cac cac acc tat ctt gta agt ccc tgt agt aat aaa ata   384
Ser Leu Ser His His Thr Tyr Leu Val Ser Pro Cys Ser Asn Lys Ile
        115                 120                 125

tat cct gaa tat ttt act gga ggt gaa ctg ttt gaa gac ata gtg gca   432
Tyr Pro Glu Tyr Phe Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala
    130                 135                 140

aga gaa tac tac agt gaa gct gat gcc agt cat tgc att cag cag atc   480
Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile
145                 150                 155                 160

ctg gag gct gtg cta cac tgc cat cag atg ggc gtg gtc cat cgg gac   528
Leu Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg Asp
                165                 170                 175

ctg aag cct gag aat ttg ctt tta gct agc aaa tcc aag gga gca gct   576
Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala
            180                 185                 190

gtg aaa ttg gca gac ttt ggc tta gcc ata gaa gtt caa ggg gac cag   624
Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln
        195                 200                 205
```

```
cag gcg tgg ttt ggt ttt gct ggc aca cct gga tat ctt tct cca gaa   672
Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu
    210                 215                 220

gtt tta cgt aaa gat cct tat gga aag cca gtg gat atg tgg gca tgt   720
Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys
225                 230                 235                 240

ggt gtc att ctc tat att cta ctt gtg ggg tat cca ccc ttc tgg gat   768
Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp
                245                 250                 255

gaa gac caa cac aga ctc tat cag cag atc aag gct gga gct tat gat   816
Glu Asp Gln His Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp
            260                 265                 270

ttt cca tca cca gaa tgg gac acg gtg act cct gaa gcc aaa gac ctc   864
Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu
        275                 280                 285

atc aat aaa atg ctt act atc aac cct gcc aaa cgc atc aca gcc tca   912
Ile Asn Lys Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser
    290                 295                 300

gag gca ctg aag cac cca tgg atc tgt caa cgt tct act gtt gct tcc   960
Glu Ala Leu Lys His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser
305                 310                 315                 320

atg atg cac aga cag gag act gta gac tgc ttg aag aaa ttt aat gct   1008
Met Met His Arg Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala
                325                 330                 335

aga aga aaa cta aag ggt gcc atc ttg aca act atg ctg gct aca agg   1056
Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg
            340                 345                 350

aat ttc tca ggt aca tgc att ggg aac tct gct tct tat ccc ttg gag   1104
Asn Phe Ser Gly Thr Cys Ile Gly Asn Ser Ala Ser Tyr Pro Leu Glu
        355                 360                 365

ccc caa act act gta atc cac aac cct gat gga aac aag gag tca act   1152
Pro Gln Thr Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr
    370                 375                 380

gag agt tca aat aca aca att gag gat gaa gat gtg aaa gaa gaa ggt   1200
Glu Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Glu Glu Gly
385                 390                 395                 400

ata act aga ata acc aat aca gag aag tgc tta aag gag ctg atg gag   1248
Ile Thr Arg Ile Thr Asn Thr Glu Lys Cys Leu Lys Glu Leu Met Glu
                405                 410                 415

ctg aaa acc aag gct caa gaa cta cgt gaa gaa tgc aga agc ctc agg   1296
Leu Lys Thr Lys Ala Gln Glu Leu Arg Glu Glu Cys Arg Ser Leu Arg
            420                 425                 430

agc cga tgc gat caa ctg gaa gaa agg gtg tca gtg atg gaa gat gaa   1344
Ser Arg Cys Asp Gln Leu Glu Glu Arg Val Ser Val Met Glu Asp Glu
        435                 440                 445
```

```
atg aat gaa atg aag caa gaa ggg aag ttt aga gaa aaa aga ata aaa   1392
Met Asn Glu Met Lys Gln Glu Gly Lys Phe Arg Glu Lys Arg Ile Lys
    450                 455                 460

aga aat gag caa agc                                              1407
Arg Asn Glu Gln Ser
465
```

<210> 74
<211> 469
<212> PRT
<213> Homo sapiens

<400> 74

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Lys Gly Val Gly Arg Phe Lys Asp Arg Lys Tyr Glu Ile Ile Arg Phe
 1               5                  10                  15
His Tyr Thr Lys Leu Ser Leu Ala Ala Val Trp Gln Gly Ile Ile Gly
            20                  25                  30
Gly Gln Asn Gly Ser Gly Gly Lys Trp Ile Leu Glu Glu Ser Lys Lys
        35                  40                  45
Lys Asn Asp Asn Asp Leu Gly Ile Gly Glu Ser Ser Arg Gly Glu Asn
    50                  55                  60
Leu Cys Phe Ile Phe Lys Ser Ser Val Arg Val Cys His Val Met Glu
65                  70                  75                  80
Val His Ala Tyr Thr Gly Ser His Tyr Val Ala Gln Thr Glu Phe Leu
                85                  90                  95
Gly Ser Ser Asp Pro Pro Ala Leu Ala Ser Gln Asn Ala Glu Val Thr
            100                 105                 110
Ser Leu Ser His His Thr Tyr Leu Val Ser Pro Cys Ser Asn Lys Ile
        115                 120                 125
Tyr Pro Glu Tyr Phe Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala
    130                 135                 140
Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile
145                 150                 155                 160
Leu Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg Asp
                165                 170                 175
Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala
            180                 185                 190
Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln
        195                 200                 205
Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu
    210                 215                 220
Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys
225                 230                 235                 240
Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp
                245                 250                 255
Glu Asp Gln His Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp
            260                 265                 270
Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu
        275                 280                 285
Ile Asn Lys Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser
    290                 295                 300
Glu Ala Leu Lys His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser
305                 310                 315                 320
Met Met His Arg Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala
                325                 330                 335
Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg
            340                 345                 350
Asn Phe Ser Gly Thr Cys Ile Gly Asn Ser Ala Ser Tyr Pro Leu Glu
        355                 360                 365
```

```
Pro Gln Thr Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr
    370                 375                 380
Glu Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Glu Glu Gly
385                 390                 395                 400
Ile Thr Arg Ile Thr Asn Thr Glu Lys Cys Leu Lys Glu Leu Met Glu
                405                 410                 415
Leu Lys Thr Lys Ala Gln Glu Leu Arg Glu Glu Cys Arg Ser Leu Arg
            420                 425                 430
Ser Arg Cys Asp Gln Leu Glu Glu Arg Val Ser Val Met Glu Asp Glu
        435                 440                 445
Met Asn Glu Met Lys Gln Glu Gly Lys Phe Arg Glu Lys Arg Ile Lys
    450                 455                 460
Arg Asn Glu Gln Ser
465


<210> 75
<211> 1833
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1833)
<223> MOOSE03376

<400> 75
atg gag tcg ctg gtt ttc gcg cgg cgc tcc ggc ccc act ccc tcg gcc   48
Met Glu Ser Leu Val Phe Ala Arg Arg Ser Gly Pro Thr Pro Ser Ala
 1               5                  10                  15

gca gag cta gcc cgg ccg ctg gcg gaa ggg ctg atc aag tcg ccc aag   96
Ala Glu Leu Ala Arg Pro Leu Ala Glu Gly Leu Ile Lys Ser Pro Lys
            20                  25                  30

ccc cta atg aag aag cag gcg gtg aag cgg cac cac cac aag cac aac   144
Pro Leu Met Lys Lys Gln Ala Val Lys Arg His His His Lys His Asn
        35                  40                  45

ctg cgg cac cgc tac gag ttc ctg gag acc ctg ggc aaa ggc acc tac   192
Leu Arg His Arg Tyr Glu Phe Leu Glu Thr Leu Gly Lys Gly Thr Tyr
    50                  55                  60

ggg aag gtg aag aag gcg cgg gag agc tcg ggg cgc ctg gtg gcc atc   240
Gly Lys Val Lys Lys Ala Arg Glu Ser Ser Gly Arg Leu Val Ala Ile
65                  70                  75                  80

aag tca atc cgg aag gac aaa atc aaa gat gag caa gat ctg atg cac   288
Lys Ser Ile Arg Lys Asp Lys Ile Lys Asp Glu Gln Asp Leu Met His
                85                  90                  95

ata cgg agg gag att gag atc atg tca tca ctc aac cac cct cac atc   336
Ile Arg Arg Glu Ile Glu Ile Met Ser Ser Leu Asn His Pro His Ile
            100                 105                 110

att gcc atc cat gaa gtg ttt gag aac agc agc aag atc gtg atc gtc   384
Ile Ala Ile His Glu Val Phe Glu Asn Ser Ser Lys Ile Val Ile Val
        115                 120                 125

atg gag tat gcc agc cgg ggc gac ctt tat gac tac atc agc gag cgg   432
Met Glu Tyr Ala Ser Arg Gly Asp Leu Tyr Asp Tyr Ile Ser Glu Arg
    130                 135                 140
```

```
cag cag ctc agt gag cgc gaa gct agg cat ttc ttc cgg cag atc gtc   480
Gln Gln Leu Ser Glu Arg Glu Ala Arg His Phe Phe Arg Gln Ile Val
145                 150                 155                 160

tct gcc gtg cac tat tgc cat cag aac aga gtt gtc cac cga gat ctc   528
Ser Ala Val His Tyr Cys His Gln Asn Arg Val Val His Arg Asp Leu
                165                 170                 175

aag ctg gag aac atc ctc ttg gat gcc aat ggg aat atc aag att gct   576
Lys Leu Glu Asn Ile Leu Leu Asp Ala Asn Gly Asn Ile Lys Ile Ala
            180                 185                 190

gac ttc ggt ctc tcc aac ctc tac cat caa ggc aag ttc ctg cag aca   624
Asp Phe Gly Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr
        195                 200                 205

ttc tgt ggg agc ccc ctc tat gcc tcg cca gag att gtc aat ggg aag   672
Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile Val Asn Gly Lys
    210                 215                 220

ccc tac aca ggc cca gag gtg gac agc tgg tcc ctg ggt gtt ctc ctc   720
Pro Tyr Thr Gly Pro Glu Val Asp Ser Trp Ser Leu Gly Val Leu Leu
225                 230                 235                 240

tac atc ctg gtg cat ggc acc atg ccc ttt gat ggg cat gac cat aag   768
Tyr Ile Leu Val His Gly Thr Met Pro Phe Asp Gly His Asp His Lys
                245                 250                 255

atc cta gtg aaa cag atc agc aac ggg gcc tac cgg gag cca cct aaa   816
Ile Leu Val Lys Gln Ile Ser Asn Gly Ala Tyr Arg Glu Pro Pro Lys
            260                 265                 270

ccc tct gca cct gcc ttt tgt ctt cca gat gcc tgt ggc ctg atc cgg   864
Pro Ser Ala Pro Ala Phe Cys Leu Pro Asp Ala Cys Gly Leu Ile Arg
        275                 280                 285

tgg ctg ttg atg gtg aac ccc acc cgc cgg gcc acc ctg gag gat gtg   912
Trp Leu Leu Met Val Asn Pro Thr Arg Arg Ala Thr Leu Glu Asp Val
    290                 295                 300

gcc agt cac tgg tgg gtc aac tgg ggc tac gcc acc cga gtg gga gag   960
Ala Ser His Trp Trp Val Asn Trp Gly Tyr Ala Thr Arg Val Gly Glu
305                 310                 315                 320

cag gag gct ccg cat gag ggt ggg cac cct ggc agt gac tct gcc cgc   1008
Gln Glu Ala Pro His Glu Gly Gly His Pro Gly Ser Asp Ser Ala Arg
                325                 330                 335

gcc tcc atg gct gac tgg ctc cgg cgt tcc tcc cgc ccc ctc ctg gag   1056
Ala Ser Met Ala Asp Trp Leu Arg Arg Ser Ser Arg Pro Leu Leu Glu
            340                 345                 350

aat ggg gcc aag gtg tgc agc ttc ttc aag cag cat gca cct ggt ggg   1104
Asn Gly Ala Lys Val Cys Ser Phe Phe Lys Gln His Ala Pro Gly Gly
        355                 360                 365

gga agc acc acc cct ggc ctg gag cgc cag cat tcg ctc aag aag tcc   1152
Gly Ser Thr Thr Pro Gly Leu Glu Arg Gln His Ser Leu Lys Lys Ser
    370                 375                 380
```

```
cgc aag gag aat gac atg gcc cag tct ctc cac agt gac acg gct gat   1200
Arg Lys Glu Asn Asp Met Ala Gln Ser Leu His Ser Asp Thr Ala Asp
385                 390                 395                 400

gac act gcc cat cgc cct ggc aag agc aac ctc aag ctg cca aag ggc   1248
Asp Thr Ala His Arg Pro Gly Lys Ser Asn Leu Lys Leu Pro Lys Gly
                405                 410                 415

att ctc aag aag aag gtg tca gcc tct gca gaa ggg gta cag gag gac   1296
Ile Leu Lys Lys Lys Val Ser Ala Ser Ala Glu Gly Val Gln Glu Asp
            420                 425                 430

cct ccg gag ctc agc cca atc cct gcg agc cca ggg cag gct gcc ccc   1344
Pro Pro Glu Leu Ser Pro Ile Pro Ala Ser Pro Gly Gln Ala Ala Pro
        435                 440                 445

ctg ctc ccc aag aag ggc att ctc aag aag ccc cga cag cgc gag tct   1392
Leu Leu Pro Lys Lys Gly Ile Leu Lys Lys Pro Arg Gln Arg Glu Ser
    450                 455                 460

ggc tac tac tcc tct ccc gag ccc agt gaa tct ggg gag ctc ttg gac   1440
Gly Tyr Tyr Ser Ser Pro Glu Pro Ser Glu Ser Gly Glu Leu Leu Asp
465                 470                 475                 480

gca ggc gac gtg ttt gtg agt ggg gat ccc aag gag cag aag cct ccg   1488
Ala Gly Asp Val Phe Val Ser Gly Asp Pro Lys Glu Gln Lys Pro Pro
                485                 490                 495

caa gct tca ggg ctg ctc ctc cat cgc aaa ggc atc ctc aaa ctc aat   1536
Gln Ala Ser Gly Leu Leu Leu His Arg Lys Gly Ile Leu Lys Leu Asn
            500                 505                 510

ggc aag ttc tcc cag aca gcc ttg gag ctc gcg gcc ccc acc acc ttc   1584
Gly Lys Phe Ser Gln Thr Ala Leu Glu Leu Ala Ala Pro Thr Thr Phe
        515                 520                 525

ggc tcc ctg gat gaa ctc gcc cca cct cgc ccc ctg gcc cgg gcc agc   1632
Gly Ser Leu Asp Glu Leu Ala Pro Pro Arg Pro Leu Ala Arg Ala Ser
    530                 535                 540

cga ccc tca ggg gct gtg agc gag gac agc atc ctg tcc tct gag tcc   1680
Arg Pro Ser Gly Ala Val Ser Glu Asp Ser Ile Leu Ser Ser Glu Ser
545                 550                 555                 560

ttt gac cag ctg gac ttg cct gaa cgg ctc cca gag ccc cca ctg cgg   1728
Phe Asp Gln Leu Asp Leu Pro Glu Arg Leu Pro Glu Pro Pro Leu Arg
                565                 570                 575

ggc tgt gct cat tat acc tcc tgc cac atc tat atc aac agc ccc tgt   1776
Gly Cys Ala His Tyr Thr Ser Cys His Ile Tyr Ile Asn Ser Pro Cys
            580                 585                 590

acc cca aca tct aac cag aag ccc cga ctt cac agg gtc agt gga gaa   1824
Thr Pro Thr Ser Asn Gln Lys Pro Arg Leu His Arg Val Ser Gly Glu
        595                 600                 605

tca ata aaa                                                      1833
Ser Ile Lys
    610
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<210> 76

<211> 611
<212> PRT
<213> Homo sapiens

<400> 76
Met Glu Ser Leu Val Phe Ala Arg Arg Ser Gly Pro Thr Pro Ser Ala
1 5 10 15
Ala Glu Leu Ala Arg Pro Leu Ala Glu Gly Leu Ile Lys Ser Pro Lys
20 25 30
Pro Leu Met Lys Lys Gln Ala Val Lys Arg His His His Lys His Asn
35 40 45
Leu Arg His Arg Tyr Glu Phe Leu Glu Thr Leu Gly Lys Gly Thr Tyr
50 55 60
Gly Lys Val Lys Lys Ala Arg Glu Ser Ser Gly Arg Leu Val Ala Ile
65 70 75 80
Lys Ser Ile Arg Lys Asp Lys Ile Lys Asp Glu Gln Asp Leu Met His
85 90 95
Ile Arg Arg Glu Ile Glu Ile Met Ser Ser Leu Asn His Pro His Ile
100 105 110
Ile Ala Ile His Glu Val Phe Glu Asn Ser Ser Lys Ile Val Ile Val
115 120 125
Met Glu Tyr Ala Ser Arg Gly Asp Leu Tyr Asp Tyr Ile Ser Glu Arg
130 135 140
Gln Gln Leu Ser Glu Arg Glu Ala Arg His Phe Phe Arg Gln Ile Val
145 150 155 160
Ser Ala Val His Tyr Cys His Gln Asn Arg Val Val His Arg Asp Leu
165 170 175
Lys Leu Glu Asn Ile Leu Leu Asp Ala Asn Gly Asn Ile Lys Ile Ala
180 185 190
Asp Phe Gly Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr
195 200 205
Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile Val Asn Gly Lys
210 215 220
Pro Tyr Thr Gly Pro Glu Val Asp Ser Trp Ser Leu Gly Val Leu Leu
225 230 235 240
Tyr Ile Leu Val His Gly Thr Met Pro Phe Asp Gly His Asp His Lys
245 250 255
Ile Leu Val Lys Gln Ile Ser Asn Gly Ala Tyr Arg Glu Pro Pro Lys
260 265 270
Pro Ser Ala Pro Ala Phe Cys Leu Pro Asp Ala Cys Gly Leu Ile Arg
275 280 285
Trp Leu Leu Met Val Asn Pro Thr Arg Arg Ala Thr Leu Glu Asp Val
290 295 300
Ala Ser His Trp Trp Val Asn Trp Gly Tyr Ala Thr Arg Val Gly Glu
305 310 315 320
Gln Glu Ala Pro His Glu Gly Gly His Pro Gly Ser Asp Ser Ala Arg
325 330 335
Ala Ser Met Ala Asp Trp Leu Arg Arg Ser Ser Arg Pro Leu Leu Glu
340 345 350
Asn Gly Ala Lys Val Cys Ser Phe Phe Lys Gln His Ala Pro Gly Gly
355 360 365
Gly Ser Thr Thr Pro Gly Leu Glu Arg Gln His Ser Leu Lys Lys Ser
370 375 380
Arg Lys Glu Asn Asp Met Ala Gln Ser Leu His Ser Asp Thr Ala Asp
385 390 395 400
Asp Thr Ala His Arg Pro Gly Lys Ser Asn Leu Lys Leu Pro Lys Gly
405 410 415
Ile Leu Lys Lys Lys Val Ser Ala Ser Ala Glu Gly Val Gln Glu Asp
420 425 430
Pro Pro Glu Leu Ser Pro Ile Pro Ala Ser Pro Gly Gln Ala Ala Pro
435 440 445

```
Leu Leu Pro Lys Lys Gly Ile Leu Lys Lys Pro Arg Gln Arg Glu Ser
    450                 455                 460
Gly Tyr Tyr Ser Ser Pro Glu Pro Ser Glu Ser Gly Glu Leu Leu Asp
465                 470                 475                 480
Ala Gly Asp Val Phe Val Ser Gly Asp Pro Lys Glu Gln Lys Pro Pro
                485                 490                 495
Gln Ala Ser Gly Leu Leu Leu His Arg Lys Gly Ile Leu Lys Leu Asn
            500                 505                 510
Gly Lys Phe Ser Gln Thr Ala Leu Glu Leu Ala Ala Pro Thr Thr Phe
        515                 520                 525
Gly Ser Leu Asp Glu Leu Ala Pro Pro Arg Pro Leu Ala Arg Ala Ser
    530                 535                 540
Arg Pro Ser Gly Ala Val Ser Glu Asp Ser Ile Leu Ser Ser Glu Ser
545                 550                 555                 560
Phe Asp Gln Leu Asp Leu Pro Glu Arg Leu Pro Glu Pro Pro Leu Arg
                565                 570                 575
Gly Cys Ala His Tyr Thr Ser Cys His Ile Tyr Ile Asn Ser Pro Cys
            580                 585                 590
Thr Pro Thr Ser Asn Gln Lys Pro Arg Leu His Arg Val Ser Gly Glu
        595                 600                 605
Ser Ile Lys
    610
```

<210> 77
<211> 2346
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(2346)
<223> MOOSE03459

<400> 77

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atg atc act tat act ttg ata aaa tca tca ctt att aca ccc caa aat   48
Met Ile Thr Tyr Thr Leu Ile Lys Ser Ser Leu Ile Thr Pro Gln Asn
 1               5                  10                  15

tct gga gtc atc ttt gac tcc ccc att cag gca aga agt cat gtt ggc   96
Ser Gly Val Ile Phe Asp Ser Pro Ile Gln Ala Arg Ser His Val Gly
            20                  25                  30

tct acc ttc aaa ata tat cca aaa tca agc att tct tct tgc ctc tgt   144
Ser Thr Phe Lys Ile Tyr Pro Lys Ser Ser Ile Ser Ser Cys Leu Cys
        35                  40                  45

tct tac cac tct ggt ccc agc tgc ctt cat ctt tta tct gga tca ttc   192
Ser Tyr His Ser Gly Pro Ser Cys Leu His Leu Leu Ser Gly Ser Phe
    50                  55                  60

cag gag tcc tca aat tct tat cat tcc ctc tcc cct tgc ctc cct aca   240
Gln Glu Ser Ser Asn Ser Tyr His Ser Leu Ser Pro Cys Leu Pro Thr
65                  70                  75                  80

atc tgt tgt cag cac aac agc cac atc ctt tcc ttg cag gct tct ttt   288
Ile Cys Cys Gln His Asn Ser His Ile Leu Ser Leu Gln Ala Ser Phe
                85                  90                  95

att gtg ttt gat tct cct aga aat ttc tct gat tct cct agt cat tcc   336
Ile Val Phe Asp Ser Pro Arg Asn Phe Ser Asp Ser Pro Ser His Ser
            100                 105                 110
```

```
aaa gca aag agc ccc atg gag agg aga gcc gca ccc aga acc aag cta   384
Lys Ala Lys Ser Pro Met Glu Arg Arg Ala Ala Pro Arg Thr Lys Leu
        115                 120                 125

gag gtt tac gga ggt ctc ctc tct tcc ctg tct tcc tca ctt gtt gcc   432
Glu Val Tyr Gly Gly Leu Leu Ser Ser Leu Ser Ser Ser Leu Val Ala
    130                 135                 140

cct gtc att cgc tct gct cca gct aca cgg gct tcc ttg ctg ttc cct   480
Pro Val Ile Arg Ser Ala Pro Ala Thr Arg Ala Ser Leu Leu Phe Pro
145                 150                 155                 160

gct gtc aga cat gtt ccc cca gca cca cct gaa ggc ctc cgc ccc agt   528
Ala Val Arg His Val Pro Pro Ala Pro Pro Glu Gly Leu Arg Pro Ser
                165                 170                 175

aga agc tgc agt tct tct gtg atc cta gga aga gag aac aga tgc tca   576
Arg Ser Cys Ser Ser Ser Val Ile Leu Gly Arg Glu Asn Arg Cys Ser
            180                 185                 190

caa gcc cca ccc agt gag cag cag aag aca agc act ctg aga cca cac   624
Gln Ala Pro Pro Ser Glu Gln Gln Lys Thr Ser Thr Leu Arg Pro His
        195                 200                 205

ttt agg cca ccg gtg gga cca aaa ggg aac agg tgc ctc agc cat ccc   672
Phe Arg Pro Pro Val Gly Pro Lys Gly Asn Arg Cys Leu Ser His Pro
    210                 215                 220

aac agt gtc gtc aga ggg tcc cca ggg cat ttt cat ggc aag tac ccc   720
Asn Ser Val Val Arg Gly Ser Pro Gly His Phe His Gly Lys Tyr Pro
225                 230                 235                 240

tct gcc ccc act cca gca gtg ctt ccc aaa gtg aag cag agc tgg cag   768
Ser Ala Pro Thr Pro Ala Val Leu Pro Lys Val Lys Gln Ser Trp Gln
                245                 250                 255

gcc tta gct aca ggc tct ctc tca ggc aga tcc ctt tta aga tac ata   816
Ala Leu Ala Thr Gly Ser Leu Ser Gly Arg Ser Leu Leu Arg Tyr Ile
            260                 265                 270

cac cat gcc cac aca tcc cat gga gag aga cca atg ctt tat tct aac   864
His His Ala His Thr Ser His Gly Glu Arg Pro Met Leu Tyr Ser Asn
        275                 280                 285

tgg tca cag ggt cac cca cct agt agt gat gct tcc cag gct act ttg   912
Trp Ser Gln Gly His Pro Pro Ser Ser Asp Ala Ser Gln Ala Thr Leu
    290                 295                 300

ctg atg ctg cgt ttg ctt ctg tca ttc tgc tca acc act tcc aaa tct   960
Leu Met Leu Arg Leu Leu Leu Ser Phe Cys Ser Thr Thr Ser Lys Ser
305                 310                 315                 320

gct ttt tgt agc ctc act tct ctg cat gtt ttt tta acc ttc cac cct  1008
Ala Phe Cys Ser Leu Thr Ser Leu His Val Phe Leu Thr Phe His Pro
                325                 330                 335

cat ttc ctt atc ttg tcc cgg gag ccc ggg gcc ggc cct ggt gcg ggg  1056
His Phe Leu Ile Leu Ser Arg Glu Pro Gly Ala Gly Pro Gly Ala Gly
            340                 345                 350
```

```
tgc ggg gcc ggg agg gca ggt gcg cgc gca gcg agc ccc tcc ccc gcg   1104
Cys Gly Ala Gly Arg Ala Gly Ala Arg Ala Ala Ser Pro Ser Pro Ala
        355                 360                 365

ccc cca aag ctc ggg ggc acc ccg acc ctc ccc acg cgc ctg gcc ccg   1152
Pro Pro Lys Leu Gly Gly Thr Pro Thr Leu Pro Thr Arg Leu Ala Pro
    370                 375                 380

gcg cgg ccc tca ccc gag cgg ggg tcg aag gtg acc acg aac acg gcc   1200
Ala Arg Pro Ser Pro Glu Arg Gly Ser Lys Val Thr Thr Asn Thr Ala
385                 390                 395                 400

acc acc tgg tcc tcc tcc acc att tgt ggg acg agg gat att ccc tca   1248
Thr Thr Trp Ser Ser Ser Thr Ile Cys Gly Thr Arg Asp Ile Pro Ser
                405                 410                 415

gaa gat cag gaa aag gaa cta ttc ctt atg gaa tta ttt gcc ctc tct   1296
Glu Asp Gln Glu Lys Glu Leu Phe Leu Met Glu Leu Phe Ala Leu Ser
            420                 425                 430

aga gca cat tta tac tct caa cct gtg tca tct ttc aat aaa ttt tca   1344
Arg Ala His Leu Tyr Ser Gln Pro Val Ser Ser Phe Asn Lys Phe Ser
        435                 440                 445

aat tcc tct gct tcc aag cag aaa tgt gtt tta cga gaa acc aac atg   1392
Asn Ser Ser Ala Ser Lys Gln Lys Cys Val Leu Arg Glu Thr Asn Met
    450                 455                 460

gct tcc cgc tat gaa aaa gaa ttc ttg gag gtt gaa aaa att ggg gtt   1440
Ala Ser Arg Tyr Glu Lys Glu Phe Leu Glu Val Glu Lys Ile Gly Val
465                 470                 475                 480

ggc gaa ttt ggt aca gtc tac aag tgc att aag agg ctg gat gga tgt   1488
Gly Glu Phe Gly Thr Val Tyr Lys Cys Ile Lys Arg Leu Asp Gly Cys
                485                 490                 495

gtt tat gca ata aag cgc tct atg aaa act ttt aca gaa tta tca aat   1536
Val Tyr Ala Ile Lys Arg Ser Met Lys Thr Phe Thr Glu Leu Ser Asn
            500                 505                 510

gag aat tcg gct ttg cat gaa gtt tat gct cac gca gtg ctt ggg cat   1584
Glu Asn Ser Ala Leu His Glu Val Tyr Ala His Ala Val Leu Gly His
        515                 520                 525

cac ccc cat gtg gta cgt tac tat tcc tca tgg gca gaa gat gac cac   1632
His Pro His Val Val Arg Tyr Tyr Ser Ser Trp Ala Glu Asp Asp His
    530                 535                 540

atg atc att cag aat gaa tac tgc aat ggt ggg agt ttg caa gct gct   1680
Met Ile Ile Gln Asn Glu Tyr Cys Asn Gly Gly Ser Leu Gln Ala Ala
545                 550                 555                 560

ata tct gaa aac act aag tct ggc aat cat ttt gaa gag cca aaa ctc   1728
Ile Ser Glu Asn Thr Lys Ser Gly Asn His Phe Glu Glu Pro Lys Leu
                565                 570                 575

aag gac atc ctt cta cag att tcc ctt ggc ctt aat tac atc cac aac   1776
Lys Asp Ile Leu Leu Gln Ile Ser Leu Gly Leu Asn Tyr Ile His Asn
            580                 585                 590
```

```
tct agc atg gta cac ctg gac atc aaa cct agt aat ata ttc att tgt   1824
Ser Ser Met Val His Leu Asp Ile Lys Pro Ser Asn Ile Phe Ile Cys
        595                 600                 605

cac aag atg caa agt gaa tcc tct gga gtc ata gaa gaa gtt gaa aat   1872
His Lys Met Gln Ser Glu Ser Ser Gly Val Ile Glu Glu Val Glu Asn
    610                 615                 620

gaa gct gat tgg ttt ctc tct gcc aat gtg atg tat aaa att ggt gac   1920
Glu Ala Asp Trp Phe Leu Ser Ala Asn Val Met Tyr Lys Ile Gly Asp
625                 630                 635                 640

ctg ggc cac gca aca tca ata aac aaa ccc aaa gtg gaa gaa gga gat   1968
Leu Gly His Ala Thr Ser Ile Asn Lys Pro Lys Val Glu Glu Gly Asp
                645                 650                 655

agt cgc ttc ctg gct aat gag att ttg caa gag gat tac cgg cac ctt   2016
Ser Arg Phe Leu Ala Asn Glu Ile Leu Gln Glu Asp Tyr Arg His Leu
            660                 665                 670

ccc aaa gca gac ata ttt gcc ttg gga tta aca att gca gtg gct gca   2064
Pro Lys Ala Asp Ile Phe Ala Leu Gly Leu Thr Ile Ala Val Ala Ala
        675                 680                 685

gga gca gag tca ttg ccc acc aat ggt gct gca tgg cac cat atc cgc   2112
Gly Ala Glu Ser Leu Pro Thr Asn Gly Ala Ala Trp His His Ile Arg
    690                 695                 700

aag ggt aac ttt ccg gac gtt cct cag gag ctc tca gaa agc ttt tcc   2160
Lys Gly Asn Phe Pro Asp Val Pro Gln Glu Leu Ser Glu Ser Phe Ser
705                 710                 715                 720

agt ctg ctc aag aac atg atc caa cct gat gcc gaa cag aga cct tct   2208
Ser Leu Leu Lys Asn Met Ile Gln Pro Asp Ala Glu Gln Arg Pro Ser
                725                 730                 735

gca gca gct ctg gcc aga aat aca gtt ctc cgg cct tcc ctg gga aaa   2256
Ala Ala Ala Leu Ala Arg Asn Thr Val Leu Arg Pro Ser Leu Gly Lys
            740                 745                 750

aca gaa gag ctc caa cag cag ctg aat ttg gaa aag ttc aag act gcc   2304
Thr Glu Glu Leu Gln Gln Gln Leu Asn Leu Glu Lys Phe Lys Thr Ala
        755                 760                 765

aca ctg gaa agc agt gtt ctg aag gca ttt ttg agt aat tat           2346
Thr Leu Glu Ser Ser Val Leu Lys Ala Phe Leu Ser Asn Tyr
    770                 775                 780
```

<210> 78
<211> 782
<212> PRT
<213> Homo sapiens

<400> 78

```
Met Ile Thr Tyr Thr Leu Ile Lys Ser Ser Leu Ile Thr Pro Gln Asn
 1               5                  10                  15
Ser Gly Val Ile Phe Asp Ser Pro Ile Gln Ala Arg Ser His Val Gly
            20                  25                  30
Ser Thr Phe Lys Ile Tyr Pro Lys Ser Ser Ile Ser Ser Cys Leu Cys
        35                  40                  45
```

```
Ser Tyr His Ser Gly Pro Ser Cys Leu His Leu Leu Ser Gly Ser Phe
    50                  55                  60
Gln Glu Ser Ser Asn Ser Tyr His Ser Leu Ser Pro Cys Leu Pro Thr
65                  70                  75                  80
Ile Cys Cys Gln His Asn Ser His Ile Leu Ser Leu Gln Ala Ser Phe
                85                  90                  95
Ile Val Phe Asp Ser Pro Arg Asn Phe Ser Asp Ser Pro Ser His Ser
            100                 105                 110
Lys Ala Lys Ser Pro Met Glu Arg Arg Ala Ala Pro Arg Thr Lys Leu
        115                 120                 125
Glu Val Tyr Gly Gly Leu Leu Ser Ser Leu Ser Ser Ser Leu Val Ala
    130                 135                 140
Pro Val Ile Arg Ser Ala Pro Ala Thr Arg Ala Ser Leu Leu Phe Pro
145                 150                 155                 160
Ala Val Arg His Val Pro Pro Ala Pro Pro Glu Gly Leu Arg Pro Ser
                165                 170                 175
Arg Ser Cys Ser Ser Ser Val Ile Leu Gly Arg Glu Asn Arg Cys Ser
            180                 185                 190
Gln Ala Pro Pro Ser Glu Gln Gln Lys Thr Ser Thr Leu Arg Pro His
        195                 200                 205
Phe Arg Pro Pro Val Gly Pro Lys Gly Asn Arg Cys Leu Ser His Pro
    210                 215                 220
Asn Ser Val Val Arg Gly Ser Pro Gly His Phe His Gly Lys Tyr Pro
225                 230                 235                 240
Ser Ala Pro Thr Pro Ala Val Leu Pro Lys Val Lys Gln Ser Trp Gln
                245                 250                 255
Ala Leu Ala Thr Gly Ser Leu Ser Gly Arg Ser Leu Leu Arg Tyr Ile
            260                 265                 270
His His Ala His Thr Ser His Gly Glu Arg Pro Met Leu Tyr Ser Asn
        275                 280                 285
Trp Ser Gln Gly His Pro Pro Ser Ser Asp Ala Ser Gln Ala Thr Leu
    290                 295                 300
Leu Met Leu Arg Leu Leu Leu Ser Phe Cys Ser Thr Thr Ser Lys Ser
305                 310                 315                 320
Ala Phe Cys Ser Leu Thr Ser Leu His Val Phe Leu Thr Phe His Pro
                325                 330                 335
His Phe Leu Ile Leu Ser Arg Glu Pro Gly Ala Gly Pro Gly Ala Gly
            340                 345                 350
Cys Gly Ala Gly Arg Ala Gly Ala Arg Ala Ala Ser Pro Ser Pro Ala
        355                 360                 365
Pro Pro Lys Leu Gly Gly Thr Pro Thr Leu Pro Thr Arg Leu Ala Pro
    370                 375                 380
Ala Arg Pro Ser Pro Glu Arg Gly Ser Lys Val Thr Thr Asn Thr Ala
385                 390                 395                 400
Thr Thr Trp Ser Ser Ser Thr Ile Cys Gly Thr Arg Asp Ile Pro Ser
                405                 410                 415
Glu Asp Gln Glu Lys Glu Leu Phe Leu Met Glu Leu Phe Ala Leu Ser
            420                 425                 430
Arg Ala His Leu Tyr Ser Gln Pro Val Ser Ser Phe Asn Lys Phe Ser
        435                 440                 445
Asn Ser Ser Ala Ser Lys Gln Lys Cys Val Leu Arg Glu Thr Asn Met
    450                 455                 460
Ala Ser Arg Tyr Glu Lys Glu Phe Leu Glu Val Glu Lys Ile Gly Val
465                 470                 475                 480
Gly Glu Phe Gly Thr Val Tyr Lys Cys Ile Lys Arg Leu Asp Gly Cys
                485                 490                 495
Val Tyr Ala Ile Lys Arg Ser Met Lys Thr Phe Thr Glu Leu Ser Asn
            500                 505                 510
Glu Asn Ser Ala Leu His Glu Val Tyr Ala His Ala Val Leu Gly His
        515                 520                 525
His Pro His Val Val Arg Tyr Tyr Ser Ser Trp Ala Glu Asp Asp His
    530                 535                 540
```

```
Met Ile Ile Gln Asn Glu Tyr Cys Asn Gly Gly Ser Leu Gln Ala Ala
545                 550                 555                 560
Ile Ser Glu Asn Thr Lys Ser Gly Asn His Phe Glu Glu Pro Lys Leu
                565                 570                 575
Lys Asp Ile Leu Leu Gln Ile Ser Leu Gly Leu Asn Tyr Ile His Asn
            580                 585                 590
Ser Ser Met Val His Leu Asp Ile Lys Pro Ser Asn Ile Phe Ile Cys
        595                 600                 605
His Lys Met Gln Ser Glu Ser Ser Gly Val Ile Glu Glu Val Glu Asn
    610                 615                 620
Glu Ala Asp Trp Phe Leu Ser Ala Asn Val Met Tyr Lys Ile Gly Asp
625                 630                 635                 640
Leu Gly His Ala Thr Ser Ile Asn Lys Pro Lys Val Glu Glu Gly Asp
                645                 650                 655
Ser Arg Phe Leu Ala Asn Glu Ile Leu Gln Glu Asp Tyr Arg His Leu
            660                 665                 670
Pro Lys Ala Asp Ile Phe Ala Leu Gly Leu Thr Ile Ala Val Ala Ala
        675                 680                 685
Gly Ala Glu Ser Leu Pro Thr Asn Gly Ala Ala Trp His His Ile Arg
    690                 695                 700
Lys Gly Asn Phe Pro Asp Val Pro Gln Glu Leu Ser Glu Ser Phe Ser
705                 710                 715                 720
Ser Leu Leu Lys Asn Met Ile Gln Pro Asp Ala Glu Gln Arg Pro Ser
                725                 730                 735
Ala Ala Ala Leu Ala Arg Asn Thr Val Leu Arg Pro Ser Leu Gly Lys
            740                 745                 750
Thr Glu Glu Leu Gln Gln Gln Leu Asn Leu Glu Lys Phe Lys Thr Ala
        755                 760                 765
Thr Leu Glu Ser Ser Val Leu Lys Ala Phe Leu Ser Asn Tyr
    770                 775                 780
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<210> 79
<211> 1086
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1086)
<223> MOOSE03283

<400> 79

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ctc att gat ctt aat ggc ttc ctt atg cct agc att ctt tcg ctc aaa   48
Leu Ile Asp Leu Asn Gly Phe Leu Met Pro Ser Ile Leu Ser Leu Lys
 1               5                  10                  15

aaa tat ttc atg gag cat ttt aca ctg gtg cag agg ata cac gag act   96
Lys Tyr Phe Met Glu His Phe Thr Leu Val Gln Arg Ile His Glu Thr
            20                  25                  30

ctg tct caa aaa aca aaa aca aaa caa aaa aaa aaa caa aaa aaa aaa   144
Leu Ser Gln Lys Thr Lys Thr Lys Gln Lys Lys Lys Gln Lys Lys Lys
        35                  40                  45

aaa aaa aaa aaa aga tcg tcg atg tat gaa gtt aga agc aac cag acc   192
Lys Lys Lys Lys Arg Ser Ser Met Tyr Glu Val Arg Ser Asn Gln Thr
    50                  55                  60

acc tca cat gtc tgt tac tac tta tgt tcc cca tat tgt tct atc aca   240
Thr Ser His Val Cys Tyr Tyr Leu Cys Ser Pro Tyr Cys Ser Ile Thr
65                  70                  75                  80
```

```
ctt agg act ttg atg cac aga tgt ttg gtg gga gtg aaa atg gtt gct   288
Leu Arg Thr Leu Met His Arg Cys Leu Val Gly Val Lys Met Val Ala
                 85                  90                  95

gat gga gtg atc aaa agc gta tta tgg caa aca ctt caa gct ctt aat   336
Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln Ala Leu Asn
            100                 105                 110

ttc tgt cat ata cat aac tgt att cac aga gat ata aaa cct gaa aat   384
Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys Pro Glu Asn
        115                 120                 125

att cta ata act aag caa gga ata atc aag att tgt gac ttc ggg ttt   432
Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp Phe Gly Phe
    130                 135                 140

gca caa att ctg att cca gga gat gcc tac acc gat tat gta gct acg   480
Ala Gln Ile Leu Ile Pro Gly Asp Ala Tyr Thr Asp Tyr Val Ala Thr
145                 150                 155                 160

aga tgg tac cga gct cct gaa ctt ctt gtg gga gat act cag tat ggt   528
Arg Trp Tyr Arg Ala Pro Glu Leu Leu Val Gly Asp Thr Gln Tyr Gly
                165                 170                 175

tct tca gtc gat ata tgg gct att ggt tgt gtt ttt gca gag ctc ctg   576
Ser Ser Val Asp Ile Trp Ala Ile Gly Cys Val Phe Ala Glu Leu Leu
            180                 185                 190

aca ggc cag cca ctg tgg cct gga aaa tca gat gtg gac caa ctt tat   624
Thr Gly Gln Pro Leu Trp Pro Gly Lys Ser Asp Val Asp Gln Leu Tyr
        195                 200                 205

ctg ata atc aga aca cta gga aaa tta atc cca aga cat caa tca atc   672
Leu Ile Ile Arg Thr Leu Gly Lys Leu Ile Pro Arg His Gln Ser Ile
    210                 215                 220

ttt aaa agt aac ggg ttt ttc cat ggc atc agt ata cct gag cca gaa   720
Phe Lys Ser Asn Gly Phe Phe His Gly Ile Ser Ile Pro Glu Pro Glu
225                 230                 235                 240

gac atg gaa act ctt gag gaa aag ttc tca gat gtt cat cct gtg gct   768
Asp Met Glu Thr Leu Glu Glu Lys Phe Ser Asp Val His Pro Val Ala
                245                 250                 255

ctg aac ttc atg aag tta tta atc cag gca ggc aag gac tca gaa gcc   816
Leu Asn Phe Met Lys Leu Leu Ile Gln Ala Gly Lys Asp Ser Glu Ala
            260                 265                 270

tca att cta ctc agc tca tct caa tgc ttc aga att aag cag gac att   864
Ser Ile Leu Leu Ser Ser Ser Gln Cys Phe Arg Ile Lys Gln Asp Ile
        275                 280                 285

gct gag gca gaa gaa ttg ctt gaa cct ggg agt ttc atg tca cca aat   912
Ala Glu Ala Glu Glu Leu Leu Glu Pro Gly Ser Phe Met Ser Pro Asn
    290                 295                 300

gaa att gtt tat ccg atc ttc caa gaa atc agg aga gag aga gag aat   960
Glu Ile Val Tyr Pro Ile Phe Gln Glu Ile Arg Arg Glu Arg Glu Asn
305                 310                 315                 320
```

```
agc caa atc cct aaa cag gcc agt gat cca cct gcc ttg gcc tcc caa   1008
Ser Gln Ile Pro Lys Gln Ala Ser Asp Pro Pro Ala Leu Ala Ser Gln
                325                 330                 335

cat gct agg att aca ggt gtg agc cat cgc aca cag cca act ctt ttc   1056
His Ala Arg Ile Thr Gly Val Ser His Arg Thr Gln Pro Thr Leu Phe
            340                 345                 350

ttg aag cat tcc tct ctc aac ttc tca gac                           1086
Leu Lys His Ser Ser Leu Asn Phe Ser Asp
        355                 360
```

<210> 80
<211> 362
<212> PRT
<213> Homo sapiens

<400> 80

```
Leu Ile Asp Leu Asn Gly Phe Leu Met Pro Ser Ile Leu Ser Leu Lys
 1               5                  10                  15
Lys Tyr Phe Met Glu His Phe Thr Leu Val Gln Arg Ile His Glu Thr
            20                  25                  30
Leu Ser Gln Lys Thr Lys Thr Lys Gln Lys Lys Lys Gln Lys Lys Lys
        35                  40                  45
Lys Lys Lys Lys Arg Ser Ser Met Tyr Glu Val Arg Ser Asn Gln Thr
    50                  55                  60
Thr Ser His Val Cys Tyr Tyr Leu Cys Ser Pro Tyr Cys Ser Ile Thr
65                  70                  75                  80
Leu Arg Thr Leu Met His Arg Cys Leu Val Gly Val Lys Met Val Ala
                85                  90                  95
Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln Ala Leu Asn
            100                 105                 110
Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys Pro Glu Asn
        115                 120                 125
Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp Phe Gly Phe
    130                 135                 140
Ala Gln Ile Leu Ile Pro Gly Asp Ala Tyr Thr Asp Tyr Val Ala Thr
145                 150                 155                 160
Arg Trp Tyr Arg Ala Pro Glu Leu Leu Val Gly Asp Thr Gln Tyr Gly
                165                 170                 175
Ser Ser Val Asp Ile Trp Ala Ile Gly Cys Val Phe Ala Glu Leu Leu
            180                 185                 190
Thr Gly Gln Pro Leu Trp Pro Gly Lys Ser Asp Val Asp Gln Leu Tyr
        195                 200                 205
Leu Ile Ile Arg Thr Leu Gly Lys Leu Ile Pro Arg His Gln Ser Ile
    210                 215                 220
Phe Lys Ser Asn Gly Phe Phe His Gly Ile Ser Ile Pro Glu Pro Glu
225                 230                 235                 240
Asp Met Glu Thr Leu Glu Glu Lys Phe Ser Asp Val His Pro Val Ala
                245                 250                 255
Leu Asn Phe Met Lys Leu Leu Ile Gln Ala Gly Lys Asp Ser Glu Ala
            260                 265                 270
Ser Ile Leu Leu Ser Ser Ser Gln Cys Phe Arg Ile Lys Gln Asp Ile
        275                 280                 285
Ala Glu Ala Glu Glu Leu Leu Glu Pro Gly Ser Phe Met Ser Pro Asn
    290                 295                 300
Glu Ile Val Tyr Pro Ile Phe Gln Glu Ile Arg Arg Glu Arg Glu Asn
305                 310                 315                 320
Ser Gln Ile Pro Lys Gln Ala Ser Asp Pro Pro Ala Leu Ala Ser Gln
                325                 330                 335
```

```
His Ala Arg Ile Thr Gly Val Ser His Arg Thr Gln Pro Thr Leu Phe
            340                 345                 350
Leu Lys His Ser Ser Leu Asn Phe Ser Asp
        355                 360
```